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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

TITLE	REFERENCE AUTHORS	ORGANISM	VERSION KEYWORDS	H H F	RESULT 1		C 45		c 41	40	Jω	c 36	υ	က က သ အ 4	ωι	c 30	29 29	27	νN	c c 23	22	νN	19	c 17	بر.	13 14	c 12	c 10	ဂ	70	n Ω	.4.	N)	-	Result No. S	
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r conditions	Thompson, J.F. and	Vertebrata; Euteleostomi; ; Hominidae; Homo.		linear PAT 23-MAR-2002			AC126882 Rattus no AC106143 Rattus no	Rattus	AC111932 Rattus no AL049749 Human DNA	i i	fus mu	AC092487 Homo sapi	att	dus n	Ratt	Mou	ACUU5291 Homo sapi AC111410 Rattus no	omo	Ratt	Ratt	Rattus	Rattus	AX392431 Sequence AC111878 Rattus no	AC110189 Mus muscu	eque	AX199565 Sequence AF220208 Mus muscu	AL121913 Human DNA	AX392430 Sequence	AX071267 Sequence	AF305426 Homo sapi	domo	domo) jegue		ption	

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION
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/db_xref="taxon:9606"
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/db_xref="G1:16303742"
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GIPEPQYYAPRRFTDRLAVPPFAQRERFHRFQFTYPYLJGHEIDLEPTISLSDGEEPPP
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Emall: cgapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
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DEFINITION ACCESSION VERSION

Homo sapiens AF224278 AF224278.1

PMEPA1

protein

(PMEPA1) mR

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18-JUL-2000

SOURCE ORGANISM KEYWORDS

Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens.

Chordata; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Hominidae;

Euteleostomi; Homo

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10873380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel androgen-regulated gene, PMEPA1, 20q13 exhibits high level expression in permits 66 (3), 257-263 (2000)
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Moul,J.W. and Srivastava,
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Moul,J.W. and Srivastava,
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/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.31-13.33"
/cell_line="LNCap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="marlefyOIIIIVVVMMVNVVVITCLLSHYKLSARSFISRHSOG
RRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTY
PYLQHEIDLEPTISLSDGEEPPPYQGFCTLQLKDPEQQLELNRESVRAPPNRTIFDSD
LMDSARLGGPCPPSSNGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPP
SLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL"
a 350 c 336 g 184 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Accession Number NP_004329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="PMEPA1 protein"
/protein_id="AAF86322.1"
/db_xref="GI:9255809"
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                                                                                                                                                            /translation="MMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHREQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSS
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                                                                                                                                                                                                                                                                   145.
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                                                                                                                                                                                                                                                                                                /chromosome="20"
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AF305426
                  Submitted (13-SEP-2000)
Queensland University of
                                                                                 Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Identification and characterization of a novel gene, up-regulated in renal cell carcinoma and other solid
                                        Rae, F.K., Hooper, J.D., Direct Submission
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 61505)
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                Centre for Molecular Biotechnology, f Technology, 2 George St, Brisbane,
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YGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHTHTAPLESAAIWS
KEKDQNGHPL"
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join(321. .429,50206. .50360,56817. .56870;
/gene="STAG1/PMEPA1"
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/chromosome="20"
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/gene="STAG1/PMEPA1"
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24-FEB-2001

FEATURES SOURCE repeat repeat repeat repeat repeat	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	DEFINITION
where differences are found these are annotated as variation cogether with a note of the overlapping clone name. Note the variation annotation may not be found in the sequence submit corresponding to the overlapping clone, as we submit sequen only a small overlap as described above. The following abbreviations are used to associate primary a numbers given in the feature table with their source database. The following abbreviations are used to associate primary a numbers given in the feature table with their source database. The following abbreviations are used to associate primary a numbers given in the feature table with their source database. The following abbreviations are used to associate primary a numbers given in the feature table with their source database. The following the following fo	clonerequest@sanger.ac.uk 2000 this sequence version replaced gi:1019) guence assembly data is compared from overlan	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 130435) Sehra, H. Direct Submission Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone	island, ESTs, STSs and GSSs, complete sequence. AL03554.1 AL03554.1.15 GI:11546043 HTG; CpG island; DLM-1; macrophage protein; PCK1; phosphoenolpyruvate carboxykinase; PMEPA1; TMEPAI; transmembrane protein human. Homo sapiens	Human DNA sequence from clone RP4-718J7 on chromosome 20q13.31-13.33 Contains the PCK1 gene for soluble phosphoenolpyruvate carboxykinase 1, part of a novel gene similar to mouse DLM-1 (tumour stroma and activated macrophage protein), the 3' end of the TMEPAI gene encoding an androgen induced 1b transmembrane protein (PMEPAI), two putative novel genes, a CpG
repeat_region	, , , ,	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	repeat_region repeat_region repeat_region repeat_region	repeat_region repeat_region
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Db 128263 CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCAC 128204
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33285. .33481
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31203. .31356
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complement(21392. 21672)
/note="match: GSS: Em:AQ892114"
21667. .21775
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complement(21278.
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15028. 15111
/note="14 copies 6 mer cacaca 82% conserved"
15029. 15108
15029. 15108
15029. 15206. 4 mer acac 83% conserved"
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19211. .19290
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20413. .20463
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/note="L2 repeat: matches 2596, .2711 of consensus"
L8049, .18169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L1MB5 repeat: matches 6015. .6176 of consensus"
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| Toote="L2 repeat: matches 2661. .2739 of consensus"
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te="2 copies 32 mer 98% conserved"
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24591
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CGCCTGGCCGTGCCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTA 247	0-	188	Db
CGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCA	- 0	351	Qγ
CACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGA 187	0-	128	Db
CACAGTGTCAGGCAACGGAATCCCAGAGCCGCGAGGTCTACGCCCGCC	- a	291	Qγ
CCAGGGGCGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAG 290	$\alpha - \alpha$	231 68	Qy Db
GATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG 67	GATC	æ	Дb
GATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG 230	GATO	171	Qy
ttch 46.6%; Score 401; DB 6; Length 408; sal Similarity 100.0%; Pred. No. 2.3e-199; 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Match ocal Sim	Query Ma: Best Loca Matches	
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Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B. Human genes and gene expression products Patent: WO 0102568-A 1739 11-JAN-2001; CHIRON CORPORATION (US); HYSEQ, INC. (US)	Labai Humai Patei CHIR	TITLE JOURNAL	
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CTCTC 861	CTCTC	857	Qγ
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ACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACACACA		128023	ФФ
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AGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGC 736		677	Qy
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CCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCT 616		557 128203	Db Db

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Matches 302;
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                                                                                                                                                                                                                                                                                                  ACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCA 571
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                           Sequence
AX011709
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis and treatment of cardiovascular
Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US
Location/Qualifiers
                   AX011709.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turi, T.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 from AX392430
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                                                AX011709
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                                                                                                 286
                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                           Conservative
                                      107
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
205 c 237 g 14
                   GI:9998233
                                                                                                                                                                                                                                                                                                                                                   35.1%; Score 302; DB 6; L
100.0%; Pred. No. 2.8e-147;
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Primates;
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W00216416.
                                      W09955858
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HSJ1059L7/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 CAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCACCCTACCAGGGCCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7007305.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 812) Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenth Pilarsky,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSJ1059L7 150224 bp DNA linear PRI 24-FEI Human DNA sequence from clone RP5-1059L7 on chromosome 20q13.2-13.33 Contains the 5' end of the TMEPAI (PMEPAI) gene encoding an androgen induced 1b transmembrane protein, ESTs, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human nucleic acid sequences obtained from pancreas Patent: WO 9955858-A 107 04-NOV-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER
                                                                                                                                                                                                                                                                                                      Homo sapiens
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AL121913.4 GI:7161781
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                                                                                                                                                                                                              Skuce, C.
                                                                                                                                                                                                                                                         Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                              HTG; CpG island;
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(bases 1 to 150224)
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/db_xref="taxon:9606"
272 c 237 g 14
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                                                                                                                                                                                                                                                                            Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                              PMEPA1;
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                                                                                                                                                                                                                                                         Primates;
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Pred. No. 5.6e-131;
                                                                                                                                                                                                                                                                                                                                              TMEPAI; transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence.
                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                           Hominidae;
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GENOMFORSCHUN
                                                                                                                                                                                                                                                                              Euteleostomi;
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; TT: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 constructed by the Sanger Centre Chromosome 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-105917 is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-1059L7 The true left end of clone RP11-402F1 is at 106677 in this sequence. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: PCYPAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the library RPCI-5 constructed by the group of Pieter de Jong. For further details so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /www.chor1.org/bacpac/home.htm
                                                                                                                                                               complement(join(<2445. .2599
/gene="TMEPAI"</pre>
                                                                                                                                                                                                                                                                                                                     transmembrane protein (PMEPA1), isoform 1)"
/note="match: cDNAs: Em:AF009426 Em:AF009427 Em:AF009425
                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<2445. .2599,52376. .52477))
/gene="TMEPAI"</pre>
      /evidence=not_experimental
/product="dJ1059L7:1.1 (an
                                                                                                                                                                                                                                                   Em:AA088767"
                                                                                                                                                                                                                                                                      match: ESTs: Em:AA249792 Em:AI594390
                                                                                                                                                                                                                                                                                                           Em: AF009424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="dJ105917.1.2 (androgen induced type
transmembrane protein (PMEPA1), isoform 2)"
/protein_id="CAC32857.1"
/db_xref="GI:13160408"
                                                                    codon_start=1
                                                                                                                                                                                                              evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                          /product="dJ1059L7.1.1 (androgen induced type 1b
cransmembrane protein (PMEPA1), isoform 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
complement(join(<2445. .2599,53362. .53365))
/gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="dJ1059L7.1.2 (androgen induced type
transmembrane protein (PMEPA1), isoform 2)"
/note="match: cDNAS; Em:AF224278
match: ESTs: Em:AA088767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<2445. .2599,53362. .53425))
/gene="TMEPAI"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2616. .2707 of consensus"
complement(2445. .53425)
/gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 71. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP5-1059L7"
/clone_lib="RPCI-5"
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                                                                                          "continues in dJ718J7 (AL035541)
proteins: Tr:O15166 Tr:O15168"
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(androgen induced type 1b
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/note="match:
17902. .18039
                              /note="L2 repeat: matches 2679.
17699. .18179
                                                                                                                                    15690.
                                                                                                      68691
                                                                                                                                                 evidence=not_experimental
                                                                                                                                                                   'note="CpG island"
                                                                                                                                                                                     /note="MER20 repeat:
15096. .15497
                                                                                                                                                                                                                                  /note="23 copies 2 mer at 76% conserved"
                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1. .311 of consensus"
14448. .14493
                                                                                                                                                                                                                                                                                                                            11630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 48. .161 of consensus" complement(8858. .9277)
                                                                               note="MLT1A2 repeat: matches 1.
                                                                                                               note="MIR repeat: matches 7.
                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 11. .196 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  /note="Charlie4 repeat: matches 39. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              10035.
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9295. .9861
                                                                                                                                                                                                                                                                                             2054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TMEPAI"
                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2290.
                                                                                                                                                                                                                                                                                                                                                                                                         note="match: GSS: Em:AQ757992"
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/note="19 c
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/translation="MGVNSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQIIIIV
/VMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSS"
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/protein_id="CAB88144.1"
/db_xref="GI:7619746"
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                GSS: Em:AQ703107"
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                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 51) Shimkets,R.A. and Leach,M.D. Nucleic acids containing single nucleotide polymorph mothers of the theory of the containing single nucleotide polymorph
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WO 0151670-A 495 19-JUL-2001;
Corporation (US)
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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30974. .31029
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25208. .25295
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24752. .25042
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23439. .23512
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19070. .19291
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26450..26485
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23231. .23438
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AUTHORS
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AX392428
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Sequence 12
AX392428
                Mus
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Jolliffe,C.N., Harvey,K.F., Haines,B.P., Parasivam,G.
Identification of multiple proteins expressed in murin binding partners for the WW domains of the ubiquitin-p
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AF220208
Mus musculus
Eukaryota; Metazoa; Chordata;
                                                          AX392428.1
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                              /product="Nedd4 WW domain-binding protein 4"
/protein_id="AaG44247.1"
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GSSFQHQQSNGPSSLLEGTRLHHSHIAPLENKEKEKQKGHPL"

234 c 176 g 95 t
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/clone_lib="Novagen Cat. N
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Diagnosis and treatment of cardiovascular conditions

Patent: WO 0216416-A 12 28-FEB-2002;

THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC. (US)

Location/Qualifiers
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LRDPEQQLELNRESVRAPPNRTIFDSDLIDSTMLGGPCPPSSNSGISATCYSSGGRME
GPPPTYSEVIGHYPGSSRQHQOSNGPSSLLEGTRLHHSHIAPLENKEKEKQKCHPL"
a 305 c 247 g 147 t
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/codon_start=1
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/db_xref="taxon:10090"
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cDNA clone encodin cDNA clone encodin Human MIVR-1 homol Human breast cell Human foetal liver Probe #13688 for g Human bone marrow Probe #13051 for g Probe #8763 used t Human breast cell Human breast cell Human bone marrow Probe #3776 for ge Human bone marrow Probe #3834 for ge Human bone marrow Probe #3953 used t Probe #3953 used t Probe #3953 used t Probe #3950 used t Probe #3950 used t Probe #300 used	n polyn n MIVR- n prost n secre encodin n codi n splic e cDNA encodi

ALIGNMENTS

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RESULT 1
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cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; heart failure.
                                                                                                                                                                                                                         Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarrerioscleretic.
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CDS

Location/Qualifiers 413..1276

/*tag=

/product= "MIVR-1" /note= "This region is specifically claimed in claim

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Homo sapiens

WO200216416-A2 28-FEB-2002.

22-AUG-2000; 2000US-227159P 21-AUG-2001; 2001WO-US26089

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences AI761441.1, AI594390, CC wall, 00438 and AQ177461. Also included are expression vectors, host CC with a candidate agent, where the molecule is a nucleic acid molecule with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-cc apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and conditative as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, concars human MTVD-1
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             TACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG
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DB; AAU78231.
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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30-APR-2001;
04-MAY-2001;
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16-MAR-2001;
16-MAR-2001;
06-APR-2001;
                                                                                          Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated grare expressed in a prostate tissue
                                                              Claim 22;
                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                            EOS
                                                            Page 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer-associated
                                                                                                                                                                                                                                                                 Mack DH,
                                                                                                                                                                                                                                                                                                       BIOTECHNOLOGY INC
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2000US-0733742.

2001US-263957p.

2001US-276791p.

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2001US-288589p.
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The present invention relates cancer-associated transcript j

ion relates to methods of detecting transcript in a cell from a patient.

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a prostate The method

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comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful has 32115-ABK92263 represent prostate cancer-associated polynucleotide
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                          in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotractic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numen; nootropic; immunosuppressant; cytostatic; gene therapy; cance. peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; lentromes.
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Zhao
                                                                  C.N.S disorders.
Note: The sequen
                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
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25-APR-2000;
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                                                                       sequence
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2000US-0620312.
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                      cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; hnflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
Multiple sclerosis;
                                                                                                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                   cDNA encoding
                                                                                                                                                                                                15-JAN-2001
                                                                                                                                                                                                                             AAA75151;
                                                                                                                                                                                                                                                         AAA75151 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and the second control of the control of the control of the control of the cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and the control of the control of the cellular diseases and the control of the cellular advantage and the cellular diseases and the cellular diseases
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P-PSDB; AAB18449.
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ischemic cerebrovascular disease; stroke; cerebral neoplasm;
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                                                                                                                                                                                                                                  CC treating or preventing a disorder associated with decreased corrections or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP or their fragments or derivatives are consciular disease, stroke, cerebral neoplasms. Alzheimer's cerebrovascular disease, Huntington's disease, dementia and parkinson's disease. NEUAPs are also useful for treating other cerebral neoplasms. Alzheimer's cerebral and viral meningitis, prion diseases including kuru, Creutrieldt-Jakob disease, nutritional and cerebral including kuru, Creutrieldt-Jakob disease, nutritional and cerebral cerebral cerebral cerebral neoplasms. Alzheimer's developmental disorders of the central nervous system, cerebral cerebral nervous system, cerebral cerebral nervous system disorders, autonomic nervous system disorders, cerainal nerve disorders, peripheral nervous system disorders, cerainal nerve disorders, peripheral nervous system disorders, cerainal nerve disorders, peripheral nervous system disorders, cerainal nerve disorders such as actinic keratosis, mental disorders, peripheral nervous system disorders, ceribral cord diseases, muscular disorders, ceribral cereforms, and toxic myopathies, mental cereforms, cereforms, cereforms, and an autoimmune/inflammatory cereforms, cereforms, and an autoimmune/inflammatory cereforms, cereforms, and an autoimmune/inflammatory cereforms, and peripheral gland, bladder, bone, becast, cervix, and an autoimmune/inflammatory cereforms, and trauma. This sequence was given the Incyte ID no. 1871286BB1.
                                                                                                                                                                  Matches
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Lu DAM,
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                                                                                                                                                                                                                                  Sequence 1061 BP;
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15-JAN-2001
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CC AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular poliferation, modulate cellular differentiation and/or modulate cellular adhesion. The CC disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, cc modulate cell adhesion in proliferative disorders, such as cancer, cc modulate the proliferation, differentiation, and/or function of cells and hematopoietic associated diseases and disorders, atelectasis, cc and hematopoietic associated diseases and disorders, atelectasis, cc as ischemic heart disease, modulate treat cardiovascular disorders such as ischemic heart disease, modulate treat cardiovascular disorders such cc and/or function of bone and cartilage cells and to treat bone and/or cc artilage associated with the ovaries, and cerebral cedema, cc hydrocephalus, brain herniations, latrogenic disease, inflammations, brain herniations, latrogenic disease, cerebral concephalus and encephalitis, and treat hepatic disease, brain matrices, and cerebral cancers, conceit the present sequence does not appear in the specification; it was created using information provided.
         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 human and murine secreted proteins designated TANGO 216, 261,
266 and 267 useful as modulating agents of cellular processes,
for treating cancer -
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T; 0 other;
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Qy Qγ 밁 ΩV B 닭 QΥ В δÃ 밁 Qy Query Match Best Local S Matches 746 415 TACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCC 195 295 135 175 115 CTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGGTGGTGATC 235 75 15 Local Similarity les 746; Conserv CTGGCCGTGCCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCG ACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAG CTGGCCGTGCCGCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCG CTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGGTGATC Conservative 80.8%; Score 696; DB Pred. No. 0; 0; Mismatches 0; DB 21; Length 1; Indels 0, Gaps 294 134 74 174 414 254 354 194 234 0

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WPI; 2000-579269/54
P-PSDB; AAB18462.
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                                                                             M,
                                                                                                                             MILLENNIUM PHARM
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                                                                             Holtzman
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                                                                                                                                                                                99US-0122458.
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 6..764
                                                                             DA,
                                                                             Sharp
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disorder;
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CC AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 267, TANGO 267. The TANGO 267 modulate cellular proliferation, modulate CC polypeptides can be used to modulate cellular adhesion. The CC proteins can be used to treat any von Willebrand factor associated CC disorder, regulate extracellular matrix structuring, cellular adhesion, and coll trafficking and/or migration, modulate cellular interactions, CC modulate cell adhesion in proliferative disorders, such as cancer, CC modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, bronchial CC and hematopoietic associated diseases and disorders, spleen associated CC apilmonary congestion or oedema, emphysema, chronic bronchitis, bronchial CC asthma and bronchictasis, intestinal disorders, spleen associated CC diseases, modulate renal disorders, treat cardiovascular disorders such castischemic heart disease, modulate the proliferation, differentiation, castillage cells and to treat bone and/or function of bone and cartillage cells and to treat bone and/or function of bone and diseases or disorders. cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitts, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders note: the present sequence does not appear in the specification; it was created using information provided. Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer. Page -; English

Query Match Best Local S Matches Sequence 750; Similarity 969 Conservative BP; 210 75.5%; 99.7%; A; 317 0, Score 650; DB Pred. No. 5.8e 0; Mismatches C; 294 G; 148 T; 0 other; .8e-295; les 2; DB 21; Length Indels 0; Gaps

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Qy 밁 δÃ 밁 Qy g QΥ 밁 ρy В Qγ 밁 δõ Ф Q 밁 Q 370 310 410 130 170 490 250 350 190 290 230 70 TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGG ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCAACCGCTTCCAGCCCACCT GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG GCCAGGGGCGGAGGAGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG GCCAGGGGGGGAGAGAGACGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG ATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGG 249 549 649 489 469 409 189 69 169 309 369

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           AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 267, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated
                                                                                                                                                                                WPI;
                                                                                                                                                                                                     Barnes
                                                                                                                                                                                                                                                                                                                                                                                                                     cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; brain herniation; latrogenic disease; inflammation; meningitis; allzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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DB; AAB18463.
                                                                                                           human and murine secreted proteins designated TANGO 216, 266 and 267 useful as modulating agents of cellular proces for treating cancer -
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                                                                                                                                                                                                    M,
                                                                                      Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a human TANGO 261 polypeptide.
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6..764
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   extracellular matrix structuring,
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                                                                                                                                                                                                                                                                          Sequence
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breast cancer; lun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polynucleotide,
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CCAGGGGCGGAGGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAG
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                                                                         GATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                          al Similarity 100.
401; Conservative
                                                                                                                                                                                                                                                                          408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escobedo J,
Randazzo F,
                                                                                                                                                                                                                                                                        BP;
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99US-0142311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; colon cancer;
g cancer; cancer detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
                                                                                                                                                               46.6%; Sc.
100.0%; Pr
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Kennedy GC, Pot D, I
Dickson M, Labat I,
LW, Strache-Crain B;
                                                                                                                                                                       Score 401; DB; Pred. No. 3.9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer;
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3.9e-178;
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D. Lamson '
Lesh'
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                                                                                                                                                                                                                       Length 408;
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Leshkowitiz D;
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ID ARI596
AC A
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUC-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 3643.
                                                                                                              Novel nucleic acids and such as central nervous
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                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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DB; AAM40498.
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                                                                                                                                                                                                                                                  Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                               HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                        2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                                                                  Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
                                                                                                           polypeptides, useful system injuries -
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                                                                                                                                                                                                                                                  Chen R, Ma
, Xu C, Xue
R, Drmanac R'
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e AJ,
RT;
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Yang Y,
                                                                                                                                      for
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Zhang
                                                                                                                                      disorders
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The invention relates to the encoded polypeptides

human nucleic acids (AAM38642-AAM42213)

(AAI57798-AAI61369) with nootropic,

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                         204
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Note: The sequence data for this patent did not form part of the specification.
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                                                  J.C
                                                                   CGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTC
                                                                                 CGCCCTAGAGAGGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTC
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                                                                                                                       AAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCC
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16; Conservative
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Pred. No. 2
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                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC they are not identical to Genbank sequences AI761441.1, AI54390, CC NM_00438 and AQ177461. Also included are expression vectors, host CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of CC with a candidate agent, where the molecule is a nucleic acid molecule CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining if the anti-apoptotic activity is CC modulated and thereby identifying a modulator. The cardiac cell anti-cappototic molecules and nucleic acids of the invention are useful for CC treating, diagnosing and monitoring progression of such diseases and CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC stroke, arteriosclerosis and heart failure. The present sequence CC is one of the four Genbank sequences (AI761441.1) which are homologous to the CDNA for human MIVR-1 and which are specifically disclaimed.
                                                                                                                           Matches
                                                                                                                                            Query Match
Best Local 9
                                                           473 CCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCGGAGCAGCAGCAGCTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 101; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; heart failure; AI761441.1.
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Similarity
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                                                                                                                           Conservative
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                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                           This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombolytic; antiinflammatory; cytostatic; antibacterial; antifunga antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                      Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disords such as autoimmune, infectious, and central nervous system disorder.
                                                                                                                                                      Claim 1; Page 180; 618pp; English.
                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST
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thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
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sed sequence tag; EST; probe; chemotactic; proliferative;
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                                                                                                      to AAA43419 represent specifically claimed secreted expressed tags (SESTs), isolated from human, mouse, xenopus and rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis;
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disorders -
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RESULT 14
AAS84503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disoase), tumours, bacterial, fungal or viral infections, depression and
CC gsoriasis. AAA43420 to AAA43425 represent linker variants which are given
CC in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                              WPI;
   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                P-PSDB;
                                                                                                                                    (HYSE-)
                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                           30-MAR-2001;
                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #20307.
                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS84503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
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les 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTTCATCAGCCGGCACAGCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGA 270
                                                             2001-639362/73.
DB; ABG20316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCCGCCTCGGCCCACCGACCGCCCTGGCCGTGCCGCCCTTCGCCCAGC 249
                                                                                                                                    HYSEQ
                                                                                                         ВŢ,
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                                                                                                                                                                2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                           2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%; Score 229; DB 21; 100.0%; Pred. No. 1.9e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 85 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 G; 41 T; 0 other;
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RESULT 15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fit wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders forenesses gene manning identification of mutations.
Isolated human polynucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
                                                   WPI; 2001-451871/48.
P-PSDB; AAM00597.
                                                                                                       Shimkets
                                                                                                                                                                           07-JAN-2000; 2000US-0174962
                                                                                                                                                                                                             05-JAN-2001;
                                                                                                                                                                                                                                                19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                               WO200151670-A2
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Human; single nucleotide polymorphism; SNP;
forensic test; aberrant protein expression;
                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH89714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH89714 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1879 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 20307; 103pp; English.
                                                                                                                                        (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 CAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCCT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106;
                                                                                                                                                                                                                                                                                                                                                                                                    coding
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                                                                                                      RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                             2001WO-US00322
                                                                                                      Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                      sequence polymorphic site SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 A; 491 C; 502 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB; Pred. No. 9.1: 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                    paternity test; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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infection and diabetes -

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Search completed: March 18, 2003, 07:20:34 Job time: 215 secs
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                                                                                                                                                                                                                                                                                                             The present invention relates to human nucleic acids containing single nucleotide polymorphisms (SNPs). These can be used in forensic and paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, diabetes, Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis, glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis, meningitis, muscular disorders, dementia, neurological diseases, tuberous sclerosis, male infertility, hypercalcaemia, blood pressure disorders, osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or autoimmunity. The present sequence is a polymorphism-containing oligonucleotide fragment of the invention.
                                                                                                                                                                                                                                                                         Sequence 51 BP; 12 A; 16 C; 18 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 246; 475pp; English.
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 07:16:10; Search time 47 Seconds (without alignments) 5618.057 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-934-249-3 861

atgcaccgcttgatggggt.....aacagaaaggacaccctctc 861

Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0

Searched: 441362 segs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Issued_Patents_NA: *

Database :

/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	26	25	24	23	22	21	20	19	18	17	16	5	14	13	12	П	0	9	œ	7	0	σ	4	ω	N	_	10 H
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	21	21	21	21	21	21	21	21	21	23	Score
2.3								2.3	•								2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.7	Query Match
10348	6733	2130	1605	1189	1189	1044	1044	1028	1028	804	804	640	640	450	51	50	8252	8252	8252	8147	4659	1327	633	633	633	377	Length
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US-08-457-273B-41	US-09-124-541-2	US-07-952-800-1	US-09-124-541-3	PCT-US92-08328-4	US-07-781-034-4	US-07-974-409C-425	US-07-975-526-3	US-08-458-745-1	US-08-118-200-1	US-09-157-349-10	US-08-835-099A-10	US-09-157-349-16	US-08-835-099A-16	US-09-370-838-145	US-08-753-247-23	US-08-753-247-22	PCT-US93-11721-15	US-08-393-703-15	US-08-046-585-15	US-09-514-247A-9	US-08-264-578-10	US-08-165-315D-3	PCT-US95-05523-1	US-08-456-907-1	US-08-234-783-1	US-08-332-766A-1	ID
41,	'n	1	ω	4,	Sequence 4, Appli	425	ω	Sequence 1, Appli	1,	10,	10,	16,	16, 1	145,	23,	22,	15,	15,	15,	9, 1	10,	ω	Sequence 1, Appli	1,	۲,	Sequence 1, Appli	Description

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US-09-643-597-307 US-08-998-416-116	US-08-332-766A-30 US-09-397-787-328	US-08-142-551B-129 US-08-142-551B-130	US-09-497-933A-20	US-08-435-998-36	US-08-155-171B-36	US-09-813-781-69	US-08-435-998-28	US-08-435-998-27	US-08-155-171B-28	US-08-155-171B-27	US-08-453-265-5	US-08-246-982A-5	US-09-041-886-14	CO CO COC TIC
Sequence 307 Sequence 116	Sequence 30, Sequence 328,	Sequence 129, App Sequence 130, App	Sequence 20, A	Sequence 36, A	Sequence 36, A	Sequence 69, A	Sequence 28, A	Sequence 27, A	Sequence 28, A	Sequence 27, A	Sequence 5, Ap	Sequence 5, Ap	Sequence 14, App.	ordurate ray of

ALIGNMENTS

RESULT 1 US-08-332-766A-1

; Sequence 1, Application US/08332766A ; Patent No. 5843647 ; GENERAL INFORMATION:

Length 377; 0; Indels	Query Match 2.7%; Score 23; DB 2; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 23; Conservative 0; Mismatches
	; TOPOLOGY: linear
	()
	; LENGTH: 377 base pairs
	; INFORMATION FOR SEQ ID NO: 1:
	; TELEX: 6714627 CUSH
	; TELEFAX: (202) 801-3000
	; TELECOMMUNICATION INFORMATION:
H	; REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
	RATION
	/AGENT 1
	:-199
	; APPLICATION NUMBER: GB 9326052.9
	; CLASSIFICATION: 435
	FILING DATE: 01-NOV-1994
	APPLICATION NUMBER: US/08/332,766A
ì	LICATION DATA:
#1 25	Patentin
	COMPUTER: IBM PC COMPACIBLE
	H
	; COMPUTER READABLE FORM:
	; ZIP: 20005-3918
	; COUNTRY: U.S.A.
	Washington
	100 New York Avenue, N.W.
	ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P
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٠	: NIMBER OF SECTION: SIMPLE TANDEM REPEATS
	I: ARMOUR, J
	KUMAI TON:

0;

Gaps

Вb

123

TGGTGGTGATGATGGTGATGGTG 145

ADDRESSEE:

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RESULT 3
US-08-456-907-1
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                                                                                                                               Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                    5-08-234-783-1
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Best Local 9
                                                                                                                                                                                                                                                                            Matches
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GENERAL INFORMATION:
                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO:
                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
CORRESPONDENCE ADDRESS:
                           APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: WT1 M
TITLE OF INVENTION: Use T
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: WT1 Monoclon TITLE OF INVENTION: Use Therefor NUMBER OF SEQUENCES: 7
                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 208 GCACCGCCGCCGCCGCCG 228
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                                                                                                                                                                                                                                              26 GCACCGCCGCCGCCGCCG 46
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bak, Mary E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                                                                 INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: Spring House Corporate Cntr,
Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
DEDNESS: double
                                                                                                                                             Application US/08456907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08234783
                                                                                                                                                                                                                                                                                                                                                                                                                                                633 base pairs
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                                                                    Herlyn, Meenhard
Morris, Jennifer
Rauscher III, Frank J.
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                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                      WT1 Monoclonal Antibodies and Methods of Use Therefor
                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                        Score 21; 
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9505523
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy :
TITLE OF INVENTION: WT1 Monoclonal Antibodi-
TITLE OF INVENTION: Methods of Use Therefor
NUMBER OF SEQUENCES: 7
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Matches
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              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05523
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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REFERENCE/DOCKET NUMBER: WS'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/234,783 FILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LOCATION:
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                                                                                                                                                                                                                   19477
                                                                                                                                                                                                                                                                 SSEE: Howson and Howson
T: Spring House Corporate Cntr, PO Box 457
Spring House
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T: Spring House Corporate Cntr,
Spring House
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                                                                                                                                                                                                                                   USA
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28-APR-1994
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100.0%; Pred. No.
live 0; Mismatc
                US 08/234,783
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Gaps

ATTORNEY/AGENT INFORMATION:

Bak, Mary

REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:

31,215

WST48PCT

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US-08-165-315D-3
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TELEPHONE: 215-540-9200
TELEPAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                   TELEFAX: 201-327-1090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324707.0
FILING DATE: 2 December 1993
ATTORNEY/AGENT INFORMATION:
NAME: MAIY M. Krinsky
REGISTRATION NUMBER: 32423
                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS DOS SOFTWARE: WORD PROCESSOR CURRENT APPLICATION DATA:
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LENGTH: 633 base pairs
                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1327
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                MOLECULE TYPE:
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STATE: Con-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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APPLICANT: Roger Kalla
                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
PELECOMMUNICATION INFORMATION:
TELEPHONE: 201-324-6155
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                                            STRANDEDNESS:
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DESCRIPTION:
                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                           nucleic acid
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                               linear
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VS-08-165-315D-3
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                         TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4659 base pair
                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,953
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,578
FILING DATE: 23-JUN-1994
                                                                                                                                                                          FEATURE:
NAME/KEY:
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                                                       LOCATION: 2781..2838
OTHER INFORMATION: /function=
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STRANDEDNESS: gou
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 OTHER INFORMATION:
                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                           nucleic acid
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DUNCAN, H. Scott
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             misc_feature
2895..2958
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2781..2838
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1153..3753
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1099..1152
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1099..3753
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/function= "transmembrane domain"
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                                                          "transmembrane domain"
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1.4;
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US-08-046-585-15/c
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; LOCATION: (819)..(8147)
US-09-514-247A-9
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                                                                                                                                                                                                                                           Sequence 15, Application US/08046585 Patent No. 5453362
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
RRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09514247A Patent No. 6365361
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                                                                                                                                                                                                                      GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST
FILE REFERENCE: TANIGUCHI-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TANABE SEIYAKU CO. LTD. APPLICANT: TANIGUCHI, Tomoyasu
                                                                                                                                                                                                                                         tent No.
                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                 TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF INVENTION: HOST CELL FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                        227 CCGCCGCCGCCGCCGGGC 207
COUNTRY: USA.
ZIP: 94111-4187
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                                          STATE:
                                                                                       ADDRESSEE:
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LOCATION: 3534..35
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 2988..3045 OTHER INFORMATION: /fur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%; es 21; Conservative 0;
                                                      San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
                                       CA
                                                                 E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                   Lamarco, Kelly
Wilson, Angus
Herr, Winship
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3534..3597
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100.0%; F1
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Pred. No.
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Pred. No.
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Best Local Similarity 100.
21; Conservative
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8252 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAIN, RICHARD 36,627
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                  REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 24-FEB-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF INVENTION: HOST CELL FACTOR NUMBER OF SEQUENCES: 15
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LENGTH: 8252 base pairs
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                          NAME:
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TELEX: 910 277299
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                                                                                                                                                                                                                                                                                                                                               94111-4187
                                                                                                                                                        Osman,
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5585239
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EDNESS: double
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Herr, Winship
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                                                                                                                                                      Richard A
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100.0%; Pr
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Pred. No.
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; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-393-703-15
                                                    RESULT 11
US-08-753-247-22/c
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        Sequence 22, Application US/08753247
Patent No. 6210929
GENERAL INFORMATION:
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                                                                                                                                                                       Matches
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                2748
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 8252 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 56,627
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Herr, Winship
TITLE OF INVENTION: HOST CELL FACTOR
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MOLECULE TYPE:
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                                                                                                                                                                       Local Similarity
mes 21; Conserv
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STATE: CA
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STRANDEDNESS: double
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                                                                                                                TGGTGGTGATGATGGTGATGG 2728
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Pred. No
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40433/149
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                                                                                                      TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND
TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
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APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1995
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
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                                                                            CORRESPONDENCE ADDRESS
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                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                  149 TGATGATGGTGATGGTGGTG 168
                           CITY: Washington
                                                STREET:
                                                                                                                                                                                                                                                                                                                                              42 TGATGATGGTGATGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 22-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
20; Conserv
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D.C.
: USA
                                             E: Foley & Lardner
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                                                                                                                                                                      FISCHER, Bernhard FALKNER, Falko-Guenther DORNER, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISCHER, Bernhard
FALKNER, Falko-Guenther
DORNER, Friedrich
EIBL, Johann
                                                                                                                                                                                                                    SCHLOKAT, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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5.1;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; SOFTWARE: FastSEQ for w:
; SEQ ID NO 145
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-145
RESULT
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US-09-370-838-145/c
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                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 145, Application US/09370838 Patent No. 6444425 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C1
                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                                                                                                                                             CURRENT
                                                                                                                                                                                                                                                                                                         CURRENT
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT 1:
FILING DATE: 24-NOV-1995
ATTORNEY/AGENT INFORMATION:
14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                      77 CACCGCCGCCGCCGCCGC 58
                                                                 27 CACCGCCGCCGCCGCCG 46
                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 TGATGATGGTGATGGTGGTG 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 22-NO: CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/I
                                                                                                             Similarity
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                                                                                                Conservative
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100.0%;
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Pred. No.
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                                                                                              Mismatches
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RESULT 15
US-09-157-349-16/c
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                                                                                                                                                                            Sequence 16, Application US/09157349 Patent No. 6068990
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 083649
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 971055
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                        APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomohiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/835,05.
APPLICATION OF APPR-1997
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 083649/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHINTANI, Yasu
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomo
                                                                                                                                                                                                                                                                         145 CACCGCCGCCGCCGCCG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                     27 CACCGCCGCCGCCGCCG 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47
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Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 base pairs
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                                                                                           NOVEL PROTEINS,
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                                                                                           THEIR PRODUCTION
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Result
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Maximum DB
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length: 2000000000
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861
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             22.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_UBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptcodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptcodata/2/pubpna/USO7_NEW_PUB.seq:*
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10 US-09-783-590-3488
10 US-09-934-249-12
10 US-09-94-249-15
10 US-09-94-249-15
10 US-09-864-761-20542
10 US-09-864-761-376
10 US-09-864-761-3936
10 US-09-864-761-3936
10 US-09-864-761-20699
10 US-09-860-670-159
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US-09-796-753-55
US-10-000-256A-32
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US-09-738-885-3
US-09-864-761-17053
US-09-864-761-230
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            Sequence 71, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 3464, Appl
Sequence 3488, Ap
Sequence 17, Appl
Sequence 17, Appl
Sequence 15, Appl
Sequence 3776, Ap
Sequence 3776, Ap
Sequence 3936, Ap
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Sequence 3936, Ap
Sequence 3, Appli
Sequence 15, Appl
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US-09-864-761-1280	US-09-864-761-285	US-09-864-761-103	US-09-864-761-4432	US-09-864-761-21181	US-09-864-761-17104	US-09-983-965-3902	US-09-864-761-18042	US-09-901-152-3	US-10-005-169-3	US-09-853-386-47	US-09-864-761-6690	US-09-864-761-8390	US-09-864-761-14467	US-09-864-761-5297	US-09-864-761-2321	US-09-864-761-764	US-09-864-761-23424	US-09-864-761-25120	US-09-864-761-22072	US-09-864-761-19056	US-10-005-169-1	US-09-853-386-62	US-10-005-169-6	US-09-864-761-19900	US-09-864-761-3121
1280,	Sequence 285, App	103,	Sequence 4432, Ap	Sequence 21181, A	Sequence 17104, A	Sequence 3902, Ap	Sequence 18042, A	Sequence 3, Appli	ω ~	Sequence 47, Appl	Sequence 6690, Ap	Sequence 8390, Ap	Sequence 14467, A	Sequence 5297, Ap	Sequence 2321, Ap	Sequence 764, App	Sequence 23424, A	Sequence 25120, A	Sequence 22072, A	Sequence 19056, A	1, 2	62,	Sequence 6, Appli	Sequence 19900, A	Sequence 3121, Ap

ALIGNMENTS

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APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scott F.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS

FILE REFERENCE: PO738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 17
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; NAME/KEY: CDS
; LOCATION: (1)...(861)
US-09-934-249-3
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Patent No. US20020115081A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 861; Conservative
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 861
TYPE: DNA
ORGANISM: Homo Sapiens
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APPLICANT: Lanc
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121 TTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC 180
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                                                           TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
                                                                                                                                     Lee, Richard T.
Landschulz, Katherine
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100.0%; Pred. No. 0;
rative 0; Mismatches
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APPLICANT: Lee, Richard T.
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
CURRENT FILING CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTMARE: FastSEQ for Windows Version 3.0
EDG ID NO 1
LENGTH: 1321
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                                                                                                                                                                                                         Sequence 1, Application US/09934249 Patent No. US20020115081A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
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                                CTCCACCACACACACATCGCGCCCCTAGAGAGAGCCCATCTGGAGCAAAGAGAAGGAT
                                                                 TACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG
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Pred. No. 0;
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RESULT 3 US-10-098-841-71

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APPLICANT: Zhang, Jie

APPLICANT: Qian, Xiaohong B.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2

CURRENT APPLICATION NUMBER: US/10/098,841

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 09/598,042

PRIOR APPLICATION NUMBER: 09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

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APPLICANT:
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STH: 1066
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                                                  AGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCT
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Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
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Liu, Chenghua
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Wehrman, Tom
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Publication No. US20030027998A1
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CURRENT FILING DATE: 2001-03-01
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FILING DATE: 1999-05-14
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FILING DATE: 1999-12-29
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APPLICATION NUMBER:
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FILING DATE: 1999-06-30
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**IRNTION: SECRETED PROTEINS AND USES THEREOF

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PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR PPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-06-29
PRIOR PPLICATION NUMBER: 09/665,666
PRIOR PPLICATION NUMBER: 09/677,751
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR PRIOR PRIOR DATE: 2000-09-30
PRIOR PRIOR PRIOR DATE: 2000-09-30
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NUMBER OF SEQ ID NOS: 162
SEQ ID NO 55
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ORGANISM: Homo
FEATURE:
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FILING DATE: 2000-06-19
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APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
FILE OF INVENTION: Compositions and Methods
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 1583
TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.2%; Score 544;
100.0%; Pred. No.
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6.5e-252;
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US-09-934-249-14/c

GENERAL INFORMATION:

Sequence 14, Application US/09934249 Patent No. US20020115081A1

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US-09-783-590-3464 Application US/09783590 ; Patent no. 464, Application US/09783590 ; Patent no. 4620020110850A1 ; GENERAL INFORMATION: APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 302; Conserv
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                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 693
TYPE: DNA
ORGANISM: Homo Sapiens
FILE REFERENCE: PO-16.2C1
            TITLE OF INVENTION: Human Genes, Sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: unsure
LOCATION: (639)...(639)
OTHER INFORMATION: a, c
                                                                                                                                                                                                                                                                                                    347
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                                                                                                                                                                                                                                                                    773
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                                                                                                                                                                                                                                                                                                  ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGTGGGCCGCCCTCCTTGCTGGAGG
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                                                                                                                                                                                                                                   GG 286
                                                                                                                                                                                                                                                                  GG 774
                                                                                                                                                                                                                                                                                                                     GCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGT
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                             Rosen, Craig A.
Ruben, Steven M
                                                                Li, Haodong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.1%; 5cc
100.0%; Pr/
0;
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             and
             Expression
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             Products
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US-09-783-590-3488; Sequence 3488, Application; Patent No. US20020110850A1
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                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3464
LENGTH: 368
                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION UNMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                                        APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                           APPLICANT:
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LOCATION: (279)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (367)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (366)
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LOCATION: (350)
OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (225)
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                                                                                                                                                                                                                                                                                                                                                61 ACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
102; Conserv
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                                                                                                                                       Rosen, Craig A. Ruben, Steven M
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ilarity 100.0%;
Conservative (
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Pred. No. 1.9e-39;
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                                                                                                                     Expression Products 16.2
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APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 878
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                                                                               Sequence 57, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: MCCEATTHY, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
DETTA ADDITION NUMBER: 09/181,175
                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(841)
US-09-934-249-12
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%;
Best Local Similarity 100.0%;
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                           CURREMI FILING NUMBER: 09/1
PRIOR APPLICATION NUMBER: 09/2
PRIOR APPLICATION NUMBER: 09/2
PRIOR APPLICATION NUMBER: 1998-12-30
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Best Local S
Matches 50
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               PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Ka
APPLICANT: Turi, Thomas G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 878
TYPE: DNA
ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                     463 GGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT 506
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                                            09/223,094
                                                                          09/183,175
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                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 10;
Pred. No. 1.5e-1
                                                                                                                                                                                                                                                                                                                                                      Mismatches
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1.7e-14;
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APPLICANT: Lee, Richard APPLICANT: Landschulz,
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RESULT 11
US-09-934-249-15
; Sequence 15, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (2)...(652)
US-09-796-753-57
                                                                                                                                                                        Matches
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 57
LENGTH: 1713
                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                LENGTH: 17
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                               ORGANISM: Mouse
                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                    463 GGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT 506
                                                                                                       269 GGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT 312
                                                                                                                                                                        Local Similarity
les 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: 09/47
OR FILING DATE: 1999-12-23
OR APPLICATION NUMBER: 09/47
OR FILING DATE: 1999-12-29
OR APPLICATION NUMBER: 09/47
OR FILING DATE: 1999-12-29
OR APPLICATION NUMBER: 09/51
OR FILING DATE: 2000-02-25
OR FILING DATE: 2000-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/630,334 FILING DATE: 2000-07-31
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FILING DATE: 2000-05-14
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APPLICATION NUMBER: 09/
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AND THE 1999-07-30
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FILING DATE: 2000-03-01
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APPLICATION NUMBER: U9/J
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; ORGANISM: Mus Musculus
US-09-934-249-15
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
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PRIOR FILING DATE: 2000-09-27
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Local Similarity 100.0%;
as 41; Conservation
                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687
                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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Pred. No.
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RESULT 13
US-09-864-761-3776
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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ORGANISM: HOMO:
FEATURE:
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN FOTAL LIVER, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 5.7
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OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 5.7
OTHER INFORMATION: WT HIT: X61479.1, EVALUE 5.40e-01
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                                                                                                           OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
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                                      APPLICATION NUMBER: PCT, FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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Chen, Wensheng
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                                                                                 PCT/US01/00668
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Pred. No.
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8.4e-06
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RESULT 14
US-09-864-761-3936
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APPLICANT: Rank,
APPLICANT: Hanze
APPLICANT: Chen,
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Best Local
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: US 60/207,456
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LENGTH: 1964
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Aeomica-X-1
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PRIOR EILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo
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                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
PTITING DATE: 2001-01-30
                                                                                                                                            FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
FILING DATE:
                                            APPLICATION NUMBER: PCT/US01/00664
                                                                                                       APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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D IN HEART, SIGNAL = 3.3

D IN ADULT LIVER, SIGNAL = 3.3

D IN FETAL LIVER, SIGNAL = 3.3

D IN LUNG, SIGNAL = 4.7

ED IN BONE MARROW, SIGNAL = 5.7
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IN PLACENTA, SIGNAL = 4.5
IN BT474, SIGNAL = 4.5
IN BRAIN, SIGNAL = 5
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Pred. No.
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US-09-864-761-20699
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                                                     APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
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Best Local Similarity
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EQ ID NO 3936
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                   APPLICATION NUMBER:
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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N: EXPRESSED IN HEART, SIGNAL = 10

N: EXPRESSED IN FETAL LIVER, SIGNAL = 13

N: EXPRESSED IN HOLLO, SIGNAL = 12

N: EXPRESSED IN HELA, SIGNAL = 13

N: EXPRESSED IN HELA, SIGNAL = 13

N: EXPRESSED IN ADULT LIVER, SIGNAL = 13

N: EXPRESSED IN BRAIN, SIGNAL = 13

N: EXPRESSED IN BRAIN, SIGNAL = 13

N: EXPRESSED IN BRAIN, SIGNAL = 12

N: EXPRESSED IN BRAIN, SIGNAL = 12

N: EXPRESSED IN BONE MARROW, SIGNAL = 9.
NUMBER: PCT/US01/00666
2001-01-30
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100.0%; Pr
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Search completed: March 18, 2003, 08:17:36
Job time: 82 secs
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PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILLING DATE: 2000-06-30
PRIOR FILLING DATE: 2000-06-30
PRIOR FILLING DATE: 2000-06-30
PRIOR FILLING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20699
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                        Query Match 3.4%; Score 29; DB 10; Best Local Similarity 100.0%; Pred. No. 0.00023; Matches 29; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-01-30
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N: EXPRESSED IN HEART, SIGNAL = 10

N: EXPRESSED IN FITAL LIVER, SIGNAL = 13

N: EXPRESSED IN LUNG, SIGNAL = 12

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N: EXPRESSED IN PLACENTA, SIGNAL = 13

N: EXPRESSED IN BOULT LIVER, SIGNAL = 12

N: EXPRESSED IN BOULT SIGNAL = 9.7

N: NT HIT: AL161539.2, EVALUE 3.70e+00
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FEATURES Source			COMMENT	JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BOOTIONS
http://image.llnl.gov Plate: LLCM2493 row: g column: 18 High quality sequence stop: 571. Location/Qualifiers 1. 967	cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	<pre>Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC</pre>	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 967)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	BQ641849.1 GI:21766021	BQ641849	5', mRNA sequence.	T_8287174 NIH_MGC_43 Homo sapiens c	BQ641849 967 bp mRNA linear EST 15-JUL-2002	

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/*Clone_1ib="NIH_MGC_43"
/*Clone_1ib="NIH_MGC_43"
/*tissue_type="normal pigmented retinal epithelium"
/*Inb_Nost="PullOB (phage-resistant)"
/*note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-ODNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/db_xref="taxon:9606"
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2791 row: n column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Location/Qualifiers
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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99.7%;
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Pred. No. 9.6e-238;
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EST.
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Plate: 13 row: h column: 06
Seg primer: M13RP1 reverse primer
Location/Qualifiers
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Expressed sequence tag analysis of human retinal for Project: Retbindin, an abundant, novel retinal cDNA
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hd13h06.yl Human Retina
Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wistow G Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Eye Institute 6/331, NIH, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing of other retina-preferred gene transcripts \underline{\text{Mol}}. Vis. 8 (4), (2002) In press
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301 496 0078
/incle="Norgan: Eye; Vector: pSPORT1; Neural retina tissue /note="Norgan: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORR1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)15-3'
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hd13h06"
/clone="hd13h06"
/clone_lib="Human Retina
                                                                                                                                                                                                    /tissue_type="Retina"
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                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 617-495-8557

Fax: 617-495-8557

Fax: 617-495-8567

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu) This sequence now available from the IMAGE

(brown@fas.harvard.edu) Topic contact: info@image.llnl.gov
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Site_2: Sal 1; Starting library constructed using superScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dr priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydrovynapatite chromatographs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by hydroxyapatite chromatography and used to make
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/db_xref="taxon:9606"
/clone="IMAGE:5677341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13626 row: C column: 10
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collected to 100 (100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ954555 916 bp mRN/AGENCOURT_8825282 Lupski_sciatic_nerve IMAGE:6204609 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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                                                                                                                    /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCACGGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected 1 kb for average insert length 1.87 kb. This is a primar library non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Bayl College of Medicine) and is available through Life
                                                                                       Technologies."
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                                                                                                                                                                                                                                                                                /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
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                58.0%;
99.7%;
Score 499; DB 14;
Pred. No. 2.4e-208;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                            5', mRNA sequence.
BQ690750
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AGENCOURT_8046394 NIH_MGC_110
5', mRNA sequence
                                 cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3368 row: h column: 14
High quality sequence stop: 627.
                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 890)
                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                          human.
/organism="Homo sapiens"
                        Location/Qualifiers
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KEYWORDS
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DEFINITION

ACCESSION

prime, mRNA sequence. AL558881 LTI_NFL008_TC2

Homo 805 dq sapiens

mRNA CDNA

clone

linear

ar EST 16-FEB-2001 CS0DJ015YF12 3

GI:12903836

ORGANISM

EST AL558881.1 numan

Eukaryota; Mammalia; F Homo sapiens

Eutheria;

Chordata;
Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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                                                                                                      AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA
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/clone="IMAGE:6209341"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: potB7; Site_1: XhoI
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Pred. No. 1.8e-207;
0; Mismatches 1;
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                                                                                                                                           AGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGC
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                                                                                                                                                                              CCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCA
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                                                                                                        TCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCTCCTTGC
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Li.W.B., Gruber,C., Jessee,J. and Polayes,
Full-length cDNA libraries and normalizati
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="T cells from T cell leukemia"
/tissue_type="T cells from T cell leukemia"
/note="Vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
/mas primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
tife Technologies. Contact: Freng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"

06 a 248 c 289 g 161 t 1 others
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/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="LTI_NFL008_TC2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 482; DB 9;
Pred. No. 6.9e-201
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 805
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Best Local Similarity
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669
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                                                                                  GGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCC
AGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ575741 729 bp mRNA linear UI-H-EZ1-bbg-h-14-0-UI.S1 NCI_CGAP_Ch2 Homo sapiens UI-H-EZ1-bbg-h-14-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia) .
/note="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia) .
with a modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI_CGAP_Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                      TAG_LIB=UI-H-EZ1
TAG_TISUE=grade-2-chondrosarcoma
TAG_TISUE=arcTAATATG"
213 c 253 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UI-H-E21-bbg-h-14-0-UI"
/clone_1ib="NCI_CGAP_Ch2"
/tissue_type="Chondrosarcoma Grade
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="taxon:9606"
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                                                                                                                                                                                               54.6%;
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                                                                                                                                                                                            Score 470; DB 14;
Pred. No. 1.3e-195;
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AL517150
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Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - France
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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1 (bases 1 to 949)
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                                                                                                                                                                                                                                                                                                                                                             Email:
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 fliang4lifetech.com URL:
fliang4lifetech.com URL:
http://fulllength.invitrogen.com"
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a 289 c 330 g 183 t
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                                                       /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                           /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                          /clone_lib="LTI_NFL011_NBC1"
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/db_xref="taxon:9606"
/clone="CS0DA008YB23"
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                                       1 (bases 1 to 655)
NIH-MGC http://mgc.nci.nih.
National Institutes of Heal
Unpublished (1999)
                                                                                                                                                AGENCOURT_8046876 NIH_MGC_1105', mRNA sequence.
BQ691705
          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                  Mammalia; Eutheria;
                                                                                             Homo sapiens
Eukaryota; M
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                                Contact: Robert Strausberg,
                                                                                                                   human
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Pred. No. 1.9e-175;
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5', mRNA sequence.
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               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1280)
     NIH-MGC
                                                                     Homo sapiens
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/db_xref="taxon:9606"
/clone="IbMAGE:6208939"
/clone=lib="NHI_MGC_110"
/clone=lib="NHI_MGC_110"
/clone="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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110 Homo sapiens
                               Craniata; Vertebrata; Catarrhini; Hominidae;
                                   Hominidae;
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                                            BQ015170 782 bp mRNA linear UI-H-ED1-axw-k-20-0-UI.s1 NCI_CGAP_ED1 Homo sapiens IMAGE:5834635 3', mRNA sequence.
              BQ015170
BQ015170.1
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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Plate: LLCM2387 row: 1 column:
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHL MCC Library."
Note: this is a NHL MCC Library."

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/db_xref="taxon:9606"
/clone="IMAGE:6248217"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma,
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AGCGCCACGTGCTACGGCAGCGGCGGCGCGCATGGAGGGGGCCGCCGCCCACCTACAGCGAG
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DHIOB (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: py773-Pac
/note="Organ: Left Pubic Bone; Vector: py773-Pac
/note="Organ: Left Pubic Bone; Vector: py773-Pac
/pharmacia) with a modified polylinker; Site_1: Ecor I;
Site_2: Not I; NCI_CGAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dr
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into py773-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
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TAG_TISSUE=chondrosarcoma
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/tissue_type="Chondrosarcoma"
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/db_xref="taxon:9606"
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Pred. No. 2.3e-172;
D; Mismatches 2;
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                               365 GTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCC
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GTCAGGCAACGGAATCCCAGAGCCGCA-GTCTACGCCCCGCCTCGGCCCACCGACCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL558882 LTI_NFL008_TC2
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Genoscope - Centre National de Sequencage
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                                                                                                                                                                                                                                                                                                                                                /tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(GT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
vector fechnologies. Contact: Feng Liang Life Technologies,
life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                               http://fulllength.invitrogen.com"
310 c 260 g 126 t
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/db_xref="taxon:9606"
/clone="CSODJ015YF12"
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/sex="male"
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Pred. No. 2.3e-172;
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                                                                                                           Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M.3 Reverse.
                                                                                                                                                                                                                              Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM712680 461 bp mRNA linear EST 28 UI-E-EJ0-ahg-a-10-0-UI.rl UI-E-EJ0 Homo sapiens cDNA clone UI-E-EJ0-ahg-a-10-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
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                                                                                                                                                                                                                                                                                                                                                   discovery
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/clone="UI-E-EJO-ahg-a-10-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
                                                        1 .461
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                 Location/Qualifiers
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469 GAGCCCCCACCCTACCAGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTG 528
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                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        Bonaldo, M.F.,
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//dev_stage="fetal (life technologies) (Tl phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed according to Benaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

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                                                                   773 GGACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAG
                                            254 ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCCCCTCCTTGCTGGAGG
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Fax: 319 335 9255
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA courses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed ,
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of.
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/db_xref="taxon:9606"
/clone="UI-E-EJO-ahs-f-20-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choroid"
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- δ δ B 833
- 밁 374 AGAAGGATAAACAGAAAGGACACCCTCTC 402 AGAAGGATAAACAGAAAGGACACCCTCTC 861

Search completed: March 18, 2003, 08:14:53 Job time: 1303 secs

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Perfect score:
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Maximum DB seq length: 2000000000
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861
1 atgcaccgcttga
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS TITLE	SOURCE ORGANISM REFERENCE	RESULT 1 AX392419 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	•	4.	2 4 3	. 4. 4	- ω	37 38	c 36	u u	C 33	u w i	၁ဖ	00 ~	10	4.10	ωκ	، د ∟ ر	ο φ	8	300	Λ.Α·	ωΝ	11	oο					21	Result No.	
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.T., Kennedy,S.P., t of cardiovascular	Chordata; Craniata; Ve Primates; Catarrhini;	861 bp DNA nt W00216416.	ALIGNMENTS	AC130935	AC128769	AL772338	AC023197	AC094473 AC084804	AC097628	AF429315	AF429315	AC110189	AC110189 HS.T10591.7	AC111069 AC097603	AC117364	AP001268 BC022716	AP001013 AP001010	AF009427	AX392431 AF009425	AX392432 AF009426	AK055028	AL837509	AX011709 AX071267	AF220208	HS718J7	AF305426	AY128643	AF224278	AF305616	AX392419 AX392417	ID	COMPANIES
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IIIVVVMMVVVUTTCLLSHYKLSARSFISRHSQGRRREDALSSEGCLMPSESTVSGN
GIPEPQVYAPPRPTDRLAVPPRAQREBRHRFQPTYPYLQHEIDLPPTISLSDGEEPPP
YOGPCTLQLRDDEQQLELNRESVRAPENRTIEDSDLMDSARLGGPCPPSSNSGISATG
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/db_xref="GI:19700735"
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/db_xref="taxon:9606"
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Turi,T.G.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                              Direct Submission Centre for Molecular Biotechnology, Queensland University of Technology, 2 George St, Brisbane, 4001, Australia
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Rae, F.K., Hooper, J.D
                                                                                                                                             Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Characterization of a novel gene, STAGI/FMEPAL, upregulated renal cell carcinoma and other solid tumors Mol. Carcinog. 32 (1), 44-53 (2001)
                                                                                                               Rae, F.K., Hooper, J.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.g. Series: IRAL Plate: 29 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Submitted (15-OCT-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                     Similarity
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Agency, Vancouver,
                                                                                                     239
                    Conservative
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                                                                                                                                           /translation="MMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWP
SESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISL
SDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSS
                                                                                                LESAAIWSKEKDKQKGHPL"
350 c 311 g
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                                                                                                                               {	t NSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAP}
                                                                                                                                                                                              /product="Unknown (protein
/protein_id="AAH15918.1"
/db_xref="GI:16198475"
                                                                                                                                                                                                                                                                                               /tissue_type="Kidney, renal
/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:20374 IMAGE:4559576"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1061
                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                 note="Vector:
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99.9%;
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Primates;
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                  0;
                                   Score 839.4; DB Pred. No. 2.4e-13
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Catarrhini; Hominidae;
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                1; DB 9;
2.4e-134;
nes 1;
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                Indels
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ORGANISM

Eukaryota; Homo sapiens Homo sapiens.

Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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RESULT 5
AF224278
LOCUS
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Homo sapiens |
AF224278
AF224278.1 G:
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          GI:9255808
                            PMEPA1
                            protein
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CATCTCGCTGTCAGACGGGGAGGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT
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                                                                          CTACGCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG
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                                                                                                                                                                                                                                                                                                                                              TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT
                                            Xu,L.L., Shanmugam,N., Segawa,T., Ses
Moul,J.W. and Srivastava,S.
A novel androgen-regulated gene, PMEE
20q13 exhibits high level expression
Genomics 66 (3), 257-263 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu,L.L., Shanmugam,N., Se
Moul,J.W. and Srivastava,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20334621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQG RRREDALSSEGCLMPSESTYSGNGIPEPQVYAPPRTDRLAVPPPAQREREHRFQPTY PYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSD LMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPP SLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL"

3 350 c 336 g 184 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Accession Number NP_004329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PMEPA1"
96. .854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="PMEPA1 protein"
/protein_id="AAF86322.1"
/db_xref="GI:9255809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
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/chromosome="20"
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98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 754.2; DB 9;
Pred. No. 9.3e-120;
); Mismatches 13;
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/a,S.
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Submitted (03-JUL-2002) Department
Reserve University/Howard Hughes Me
Ave., Cleveland, OH 44106, USA
                                                                                                                                                                                                                                                                                                                                                                                         Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence Willson, J.K.V., Lu, S., Nosrati, A., Swinler, S., Beard, L., Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S
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LESAAIWSKEKDKQKGHPL"
467 c 494 g 398 t
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Eutheria; Primates;
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Medical Institute, 11001 Cedar
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                                                                      Diagnosis and treatment of cardiovascular conditions Patent: WO 0216416-A 12 28-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER
                                                                                                                                Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                            Turi, T.G.
                                                                                                               Lee, R.T., Landschulz, K.T., Kennedy, S.P.,
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Sequence 12 from Patent
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WO0216416.
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          CACCACACACACATCGCGCCCCTAGAGAGC
CATCACTCGCACATTGCCCCACTGGAGAAC
                              GETGGGCGCATGGAGGGCCGCCCCCCACCTACAGCGAGGTCATTGGCCACTACCCTGGC
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GPPPTYSEVIGHYPGSSFQHQQSNGPSSLLEGTRLHHSHIAPLENKEKEKQKGHPL"
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GGGCGGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Identification and characterization of a novel gene, up-regulated in renal cell carcinoma and other solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGN
GIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPP
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join(321. .429,50206. .50360,58817. .56870,57305.
/gene="S7AG1/PMEPA1"
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/protein_id="AAL09357.1"
/db_xref="GI:15824469"
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/gene="STAG1/PMEPA1"
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0; Mismatches 6;
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                                                                                                                                                                                                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of the sanger Centre Chromosome 20 constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                           http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP4-718J7 The true left end of clone RP5-1007E6 is at 71437 in this sequence. The true right end of clone RP4-579F20 is at 43945 in this sequence.
RP4-718J7 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Dec 5, 2000 this sequence version replaced gi:10198628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-FEB-2001) Sanger Centre, Hinxton,
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Mammalia; Eutheria; Primates;
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This sequence was finished as follows unless otherwise noted: all
                        VECTOR: PCYPAC2
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Catarrhini; Hominidae;
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least

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FEATURES
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/clone="RP4-718J7"
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/db_xref="taxon:9606"
/chromosome="20"
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1358. .7671
note-"Alusx repeat: matches 1.
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                             'note="AluJb repeat: matches 1.
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hte="11 cr
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hte="9 cor
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te="2
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te="18 copies 58
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4. .1371
ce="3 copies 56 mer 75% conserved"
3. .2757
ce="28 copies 50 mer 54% conserved"
                                                                                                                                                                                                                                                                                                           8. .3426
te="L1MB4 repeat: matches 6088. .6136 of consensus"
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2. .2079
ce="4 copies 57 mer 86% conserved"
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                                                  94. .10206
:e="AluJb_repeat: matches 188.
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.e="FLAM_C repeat: matches 1. .132 of consensus"
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repeat: matches 2647.
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11816. .12380 /note="LTR19B repeat: matches 1. .580 of 12519. .12813 /note="L1ND2 repeat: matches 6032. .6331 /note="match: GSS: F complement(21392. .2 /note="match: GSS: F 21667. .21775 13559. 13726
7note="3 copies 56 mer 73% conserved"
13585. 13716
7note="22 copies 6 mer ctctct 67% conserved"
13586. 13717
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13588. 13715 /note="match: GSS: Em:AQ592603" /note="match: GSS:
complement(21187. . 15026. .15109 /note="7 copie 'note="L2 repeat: matches 2159. !5420. .15721 note="3 copies 32 mer 79% conserved" 5021, .15110 20413. 20463
/roote="MIR repeat: matches 90. .143 of consensus"
complement(21005. .21672) 18312. .18438 /note="MIR repeat: matches 138. 18585. .18776 complement(21278 note="L2 repeat: matches 2596. .8049. .18169 /note="16 copies 2 mer tc 87% conserved" /note="MIR repeat: 23577. .23646 /note="2_copies 35 'note="match: note="MIR repeat: matches 72. .154 of consensus" :0413. .20463 note="MER20 repeat: matches 7. 9211. .19290 note="MIR repeat: matches 86. .211 of consensus" note="Alusx repeat: matches 1. .303 of consensus" /note="FLAM_C 31203. .31356 /note="MIR repeat: matches 38. note="L1MB5 repeat: matches 6015. .6176 of 2224. .32522 note="L2_repeat: matches 2336. te="20 copies 4 mer acac 83% conserved" 73. .15399 e="45 copies 2 mer ac 80% conserved" e="2 copies 32 mer 98% conserved" 5. .16690 e="14 copies 6 mer cacaca 82% conserved" e="LTR16C te="L2 repeat: matches 2661. .15110 "7 copies 12 .15111 .15108 .14437 .13724 .16396 .26643 *2 copies 35 : .24591 .25611 .2804 27684 repeat: matches 1. repeat: matches 257. .386 of consensus* GSS: repeat: matches 1. Em: AQ748384".21672) mer 82% conserved" mer 100% conserved" matches 73. .192 of Em: AQ776209" Em: AQ892114" 21663) Em: AQ136459" .310 of consensus" .242 of consensus .250 of consensus" .2711 of consensus .2285 of consensus .2710 of .217 of consensus" .2739 of .127 of consensus " .6331 of consensus" consensus" consensus" consensus" consensus" consensus"

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Sequence 14
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Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER
Location/Qualifiers
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Mammalia; Eutheria;
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33285. .33481
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AF220208
                                                                                                               Submitted (30-DEC-1999) Division of Haematology, Hanson Centre Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia
                                                                                                                                        Jolliffe, C.N. and Kumar, S. Direct Submission
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                        /organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Novagen Cat. N
/dev_stage="16 day embryo"
<1. 609
/note="N4WBP4"
/codon_start=1
                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Kumar,S.

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Bukaryota; Metazoa; Chordata; C
Mammalla; Eutheria; Primates; C
1 (bases 1 to 812)
Schmitt,A., Specht,T., Dahl,E.,
Pilarsky,C.
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/protein_id="AAG44247.1"
/db_xref="G1:12004974"
/translation="SQARRRDDGISSEGCLWPSESTVSGGMPEPQVYAPPRPTDRLAV
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PREFIQRSRFQPTYPYLOHBIALPFTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRES
VRAPPNRFIFDSDLIDSTMLGGPCPPSSNSGISATCYSSGGRWEGPPPTYSEVIGHYP
GSSFQHQQSNGPSSLLEGTRLHHSHTAPLENKEKEKQKGHPL"
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Pred. No. 1.2e-62;
); Mismatches 80;
                                                                                                        812 bp
W09955858.
                        Craniata; Vertebrata; Catarrhini; Hominidae;
     Hinzmann, B.,
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                          Hominidae;
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   Rosenthal, A.
                                   Euteleostomi;
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SM Homo Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hon

E 1 (bases 1 to 408)

S Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Kli
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, I
Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dicker
Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache
Human genes and gene expression products

L Patent: Wo 010256-A 1739 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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/db_xref="taxon:9606"
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                                       Strache-Crain, B.
                                                   Dickson, M.,
                                                             Pot,D.,
                                                                                                          Euteleostomi;
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                                                                      Klinger, J.,
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                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 155649 bases at least Q40
Consensus quality: 155716 bases at least Q30
Consensus quality: 155743 bases at least Q20
Insert size: 155775; sum-of-contigs
Insert size: 162242; 2.6% error; agarose-fp
                                                                                                                                                                                                                                 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL837509 156075 bp DNA
Mus musculus chromosome 2 clone RP23-44L6,
PROGRESS ***, 4 unordered pieces.
                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                 Center project name: bM44L6
                                                                                                                                                                                Web site:
                                                                                                                                                                                                 Center code: SC
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/db_xref="taxon:9606"
159 c 115 g 5
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                                                                                                                                                                                http://www.sanger.ac.uk
                                                                                                                 --- Summary Statistics
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99.8%;
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Pred. No. 3e
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3e-59;
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  730 TTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCAC 789
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                                                                                                                                    GCCCCTGTCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACCTGCTACAGCAGCGGTGGG 134360
                                              CGCATGGAGGGGCCGCCCCCACCTACAGCGAGGTCATTGGCCACTACCCTGGCTCCTCC 134300
                                                                                        CGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCC 729
                                                                                                                                                         --CCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGG 669
                                                                                                                                                                                                                        Quality coverage: 7.64x in Q20 bases; sum-of-contigs Quality coverage: 7.40x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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9982 10081: gap of 100 bp
10082 13090: contig of 3009 bp in length
13091 13190: gap of 100 bp
13191 95958: contig of 82768 bp in length
95959 96058: gap of 100 bp
96059 156075: contig of 60017 bp in length
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fragment_chain:1"
. 38474 c 39272 g 38695 t
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fragment_chain:1"
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/db_xref="taxon:10090"
/chromosome="2"
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fragment_chain:1"
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82.6%;
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Pred. No. 4.2e-52;
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CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCGTCGTGGTGGTGC 694
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AF009424
AF009424.1 GI:22714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8494)
Yoshikawa,T., Sanders,A.R., Esterling,L.E., Overhauser,J., Garnes,J.A., Lennon,G., Grewal,R. and Detera-Wadleigh,S.D. Isolation of chromosome 18-specific brain transcripts as pc candidates for bipolar disorder
Am. J. Med. Genet. 74 (2), 140-149 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 8494)
Yoshikawa,T., Sanders,A.R., Esterling,L.E. and Detera-Wadleigh,S.D.
Multiple transcriptional variants and RNA editing in Cl8orfl, a
novel gene with LDLRA and transmembrane domains on 18p11.2
Genomics 47 (2), 246-257 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUN-1997) Clinical Neurogenetics Branch, National Institute of Mental Health, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 8494)
Yoshikawa, T. and Detera-Wadleigh, S.D.
                                                                                                            Similarity
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                                                                                         Conservative
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                                                                                                                                                                       /Translation="megagroatnaffeckffctsgkclyldgslucnoondcgdnsde encll/tehpppgifnselefaqiiiivvvvtvmvvvvtvcllnhykvstrsfinrpnq srredglpogeclwesdsaaprlgassimhaprsrdbftasfiqrdrfsroptyp yvqhetulpptislsdgeepppyggpctlqldpdeqomelnresvrappnrtifdsdl idlamysggpcppssnsgisasycssncrmegppptysevmghpgasflhhqrsnah rgsrlqpqqunaestivpikgkdrkpgnly" 2 others
                                                                                                                                                                                                                                                                                                                                                                                   membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                /protein_id="AAC52023.1"
/db_xref="GI:2271469"
                                                                                                                                                                                                                                                                                                                                                                                 /note="alternatively spliced; membrane-spanning protein"
                                                                                                                                                                                                                                                                                                                                                  /product="clone 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                        40.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8494 bp mRNA linear PRI 17-FEB-
22 mRNA, alternative splice variant alpha-1,
                                                                                   Score 352.2; DB 9;
Pred. No. 5.7e-51;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GAACAAGGAGAAGGAGAAACAGAAA 134195
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                                                                                                                                                      CCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC 573
                                                                                                                                                                                                 CTGTCAGACGGGGAGGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 513
                                                                                                                                                                                                                                                                                         CCGCCTCGGCCCACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCACCAGCAGCAGCAG 749
                                                        TTCGACAGTGACCTGATGGATAGTGCCAGG---CTGGGCGGCCCCTGCCCCCCCAGCAGT 630
                                                                                                                                                                                                                                 CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC 988
                                                                                                                                                                                                                                              ACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAGCGCAG
                                           AACTCGGGCATCAGTGCAAGCACCTGCAGCAGTAACGGGAGGATGGAGGGGCCACCCCC
                                                                                                                                       CTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCCTGCACCCTGCAGCTCCGGGAC 1048
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Search completed: March 17, 2003, 15:53:56 Job time: 2748.78 secs

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Maximum DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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 ABK12137
AAA75151
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AAA75163
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AAA47429
AAI57868
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8272.492 Million cell updates/sec
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                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                  ABK12137;
                22-AUG-2000; 2000US-227159P
                                          21-AUG-2001; 2001WO-US26089
                                                                                                    WO200216416-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                       28-FEB-2002
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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	ω	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
47.4	47.4	47.4	7.	47.8	æ	48.4	49	$\overline{}$	50.6	$\hat{}$	51	51.2	223.4	223.4	232	252.6	281	284.2	284.2	320.4	333.8	341.8	349	349	350				.7	.51			460.6		612.4
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22	20	21	15	20	22	20	24	23	23	23	22	20	23	23	21	23	19	24	23	23	23	24	24	19	24	21	23	22	20	24	21	21	21	21	24
AAC90084	AAZ32027		ū	AAZ17254	AAL03113	AAZ17263	ABN40872	ABL09460	ABL09373	ABL09461	AAH89714	AAX53491	AAS77313	AAS92497	AAA41265	AAS77310	AAV38336	ABK83477	AAS77305	AAS84503	AAS77312	ABK12144	ABK12145	AAV38335	425	52	730	U.	AAZ52964	ABK12143	AAA75168	16	51	515	ABK12142
Z46970 cDNA clone.	Human METH1 relate	S. lavendulae MitG	DNA encoding Pseud	Human gene express		Human gene express	0	Drosophila melanog	Drosophila melanog	βh		Human adenosine Al		DNA encoding novel	Human secreted exp	DNA encoding novel	Manic-depressive i	Human cDNA differe	DNA encoding novel	DNA encoding novel	DNA encoding novel	Human MIVR-1 homol	Human MIVR-1 homol	Manic-depressive i	Human cDNA for nov	Human secreted pro	DNA encoding novel		Human prostate tum	Human MIVR-1 homol		clone		encodi	Mouse cDNA encodin

ALIGNMENTS

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ID ABK12137 standard; cDNA; 1321 BP.

XX
AC ABK12137;
XY
AC ABK12137;
XY
DT 05-JUN-2002 (first entry)
XX
DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX
Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
XX
W cytostatic; cardiant; cerebroprotective; antiarteriosclerotic;
XX
Cardiac cell; anti-apoptotic; vascular endothelial cell;
XX
Cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
XX
W heart failure.
XX
Homo sapiens.
XX
FH Key
FT CDS

A13..1276
FT MIVR-1"

/product= "MIVR-1"
/product= "MIVR-1"
/note= "This region is specifically claimed in claim 3"
XX
PN
W0200216416-A2.
XX
PD
28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC MM_00438 and AQ177461. Also included are expression vectors, host CC cells, the MIVR-1 polypeptide. MIVR-1 binding peptides, modulators of with a candidate agent, where the molecule is a nucleic activity compression product, determining if the anti-apoptotic activity CC comprising MIVR-1, IEX-1, VDDP-1, BTG-2 and TIS-11d or its modulated and thereby identifying a modulator. The cardiac cell anti-cc apoptotic molecules and nucleic acids of the invention are useful for disorders as characterised by increased apoptotic cell-death of vascular cc andothelial cells e.g. cardiac hypertrophy, myocardial infarction, cc stroke, arteriosclerosis and heart failure. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
893 TACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCGGAGCAGCAGCTGGAACTGAACCGG
                                           481
                                                                     833
                                                                                              421
                                                                                                                          773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule encoding Mechanically Receptor-1 polypeptide, useful for treating cardic
                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
              TACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG
                                                                  CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCC
                                                    CAGCACGAGATCGACCTGCCACCATCTCGCTGTCAGACGGGGGAGGAGCCCCCACCC
                                                                                                        GTGCCGCCTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCCACCTATCCGTACCTG
                                                                                                                       GTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
                                                                                                                                                                                                                               AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
                                                                                                                                                            CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGG
                                                                                                                                                                                                                                                                                                                                        TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC
                                                                                                                                                                                                               AGGAGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
                                                                                                                                                                                                                                                                                                                         TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
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DB; AAU78231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 A; 493 C; 440 G; 165 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 861; DB 24; 100.0%; Pred. No. 2.4e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ically Induced Vascular cardiovascular diseases
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Novel human and murine
                   P-PSDB; AAB18449
                            WPI; 2000-579269/54.
                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                     01-MAR-1999;
                                                                                                        01-MAR-2000;
                                                                                                                            08-SEP-2000
                                                                                                                                                                                                                                                                    cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; historia calcandario.
                                                                                                                                              W0200052022-A1
                                                                                                                                                                            mat_peptide
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CAGCGCCACGTGCTACGGCAGCGGCGGCGCGCATGGAGGGGCCGCCGCCCACCTACAGCGA
                                                                                                                              GCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAG
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216, TANGO 262,
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for
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16-MAR-2001;
16-MAR-2001;
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08-DEC-2000;
                                                                                                                                                         Claim
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30-APR-2001;
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2001US-276791P.
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2001US-281922P.
2001US-286214P.
2001US-0847046.
2001US-288589P.
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2000US-0733742.
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in a prostate tissue
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                                             AAA75163 standard;
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                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                   identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer associated polynucleotide
                                                                                 AGAGAGCGCAGCCATCTGGAGCAAAGAAGAAGGATAAACAGAAAGGACACCCTCTC 861
                                                                                                                                                                                                                                                                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 other;
                                                                          AGAGAGCCCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTC 851
                                                                                                                                     87 TITGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT 146
                                                                                                                                                                                                 TCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAG
                                                                                                                                                                                                                                                            CATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT 506
                                                                                                                                                                                                                                                                                                                        CTACGCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCG
                                                                                                                                                                                                                                                                                                  Local Similarity
es 762; Conserv
                                                                                                                                                                                                                                                                                          AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                     ACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT 136
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.6%; Score 754.2; DB 24; Length 1140;
98.3%; Pred. No. 1.8e-145;
vative 0; Mismatches 13; Indels 0;
                                          969 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                        796
                                                                                                                                                                    676
                                                                                                                                                                                   686
                                                                                                                                                                                                                626
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                                                                                                                                                                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                                                                                                                                     266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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δã

102 GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGATGGTGAT 161

Query Match Best Local Sim Matches 756;

Similarity

87.5%; 99.5%;

Score 753.6; Pred. No. 2.3e 0; Mismatches

; DB 21; .3e-145;

Indels Length 969;

0; Gaps

0;

969 BP; 211 A; 317 C;

293

G; 148 T; 0 other;

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AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 267, TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The CC disorder, regulate extracellular matrix structuring, cellular adhesion, or modulate cell trafficking and/or migration, modulate cellular interactions, cc modulate tell adhesion in proliferative disorders, such as cancer, cc modulate the proliferation, differentiation, and/or function of cells cascolated diseases and leukocytes, treat bone marrow, and leukocytes, treat bone marrow, blood casthma and bronchiectasis, intestinal disorders, spleen associated cas ischemic heart diseases, modulate tenel diseases, modulate tenel diseases, modulate tenel diseases, modulate the proliferation, differentiation, differentiation, differentiation, chronic bronchitis, bronchial caschemic heart diseases, modulate the proliferation, differentiation, cromplysema, chronic bronchitis, bronchial caschemic heart diseases, modulate the proliferation, differentiation, cromplysema, chronic bronchitis, bronchial caschemic heart diseases, modulate the proliferation, differentiation, cromplysema, cascolated diseases, modulate the proliferation, differentiation, cromplysema, cascolated disease, and to treat bone and/or bydrocephalus, brain herniations, latrogenic disease, inflammations, cromplysema, brain the poweries, and cerebral complysema, brain cancers, constend the proliferation disease, multiple sclerosis, brain cancers, created using information provided.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-579269/54.
P-PSDB; AAB18461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1999; 99US-0122458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2000; 2000WO-US05226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267, cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; cedema; emphysema; chronic bronchitis; bronchial astima; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; haltiple sclerosis; hydrocephalus; encephalus; encephalus; encephalus; encephalus; encephalus; multiple sclerosis; hydrocephalus; encephalus; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200052022-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA clone encoding a human TANGO 261 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
6..764
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "TANGO 261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharp
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RESULT 5
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                                                                                                 TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; con willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitts; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus;
                            multiple
                                                Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA75164 standard; cDNA; 969
                                                                             brain herniation; iatrogenic disease; inflammation; meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGCACAGCCAGGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCATCGGCCACTACCCGGGGTCCTTCCTTCCAGCAGCAGAGCAGTGGGCCGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCA
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                            hydrocephalus;
                                                                                                                                                                                                                                                                                                                                  human TANGO
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                         disease;
disorder;
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282 122

CTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCG

181 281 121 221

CCGGCACAGCCAGGGGGGGGGGGGGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC

GGTGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG GGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG

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162

N

102 GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGAT 161

Gaps

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CC AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate CC proteins can be used to treat any von Willebrand factor-associated CC disorder, regulate extracellular matrix structuring, cellular adhesion, CC and cell trafficking and/or migration, modulate cellular interactions, CC modulate cell adhesion in proliferative disorders, such as cancer, CC modulate the proliferation differentiation, and/or function of cells can describe that appear in the bone marrow, and leukocytes, treat bone marrow, blood CC and hematopoietic associated diseases and disorders, atelectasis, CC pulmonary congestion or oedema, emplysema, chronic bronchitis, bronchial casthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, cas ischemic heart disease, modulate the proliferation, differentiation, cas ischemic heart diseases modulate the proliferation, differentiation, cartilage associated with the ovaries, and cerebral oedema, chydrocephalus, brain herniations, iatrogenic disease, inflammations, conscients associated with the ovaries, and cerebral oedema. Parking of the constrainty of the cartilage cells and to treat bone and/or cartilage associated with the ovaries, and cerebral oedema. Parking of disease, inflammations, conscients with the ovaries, and cerebral oedema. Parking of disease, inflammations, conscients with the ovaries, and cerebral oedema. Parking of disease, inflammations, conscients with the ovaries and cartilage cartilage carebral and cancers.
                      Best
                                        Query Match
                                                                                                                    toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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Score 753.6;
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RESULT 6
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Mismatches

87.5%; Score 753.6; 99.5%; Pred. No. 2.3

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CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The control of the cont
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210 A; 317 C; 294 G; 148 T; 0 other;
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Tang YT,
Lu DAM,
                                                                                                                          11-DEC-1998;
11-DEC-1998;
09-FEB-1999;
16-MAR-1999;
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                                                                          INCYTE PHARM INC
Yue H,
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98US-9123456.
99US-0119365.
99US-0124687.
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/product= Neuron associated protein
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CC treating or preventing a disorder associated with decreased contracting or preventing a disorder associated with decreased contracting or preventing disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression contractivity of NEUAP. NEUAP or their fragments or derivatives are conserved in the preventing disorder such as epilepsy, ischemic contracts of the cerebral disorder such as epilepsy, ischemic contracts of the cerebral neoplasms. Alzheimer's contract disease, pick's disease, huntington's disease, dementia and parkinson's disease. NEUAPs are also useful for treating other contracts of the cerebral neoplasms, alzheimer's contracts of the cerebral neoplasms, alzheimer's contracts of the central nervous system, cerebral contracts of the central nervous system, cerebral contracts of the central nervous system disorders, cerebral nervous system disorders, cerebral contracts of the central nervous system disorders, cerebral contracts of the central nervous system disorders, cerebral nervous system disorders, cerebral contracts of the central nervous system disorders, cerebral contracts of the central nervous system disorders, cerebral contracts of the central nervous system disorders, cerebral contracts of cancers undarkety and schizophrenic disorders, a cell contracts, peripheral nervous system disorders, cell contracts, cendocrine, and toxic myopathies, mental contracts, burstis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, bepatitis, mixed connective tissue disease (MCTD), myelofibrosis, bepatitis, arteriosclerosis, cervix, and an autoimmune/inflammatory contracts of the adrenal gland, bladder, bone, because of the adrenal gland, bladder, bankylosing contracts of the adrenal gland, bladder, bankylosing contracts of the certacts, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human neuron-associated proteins and polynucleotides encoding them, useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders
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Sequence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 other;

Query Match Best Local

Similarity

87.48; 98.28;

Score 752.6;

DB 21;

Length

Š В Qy В Qy В Qy 멍 Qy В QΥ B QΥ Matches 447 142 147 382 387 322 327 262 267 202 207 82 87 ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGA CATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT GGTGATGGTGGTGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT 141 TTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT 146 CTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCAC CTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT GGTGATGATGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC Conservative 0; Pred. No. 3.7e-145;); Mismatches 14; Indels 0; Gaps 446 506 441 381 386 321 261 266 0

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21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-UUL-2000; 2000US-0550042.

19-UUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0633450.

14-SEP-2000; 2000US-0663191.

19-OCT-2000; 2000US-0693136.

29-NOV-2000; 2000US-0727344.
   Novel nucleic acids and such as central nervous
                          WPI; 2001-442253/47.
P-PSDB; AAM38712.
                                                                             (HYSE-)
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                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                            HYSEQ INC.
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the encoded polypeptides (AAMM8642-AAMM42213) with nootropic, communosuppressant and cytostatic activity. The polynucleotides are useful cof in gene therapy. A composition containing a polypeptide or polynucleotide system, such as peripheral nervous injuries, peripheral nervous common containing a polypeptide or polynucleotide system, such as peripheral nervous injuries, peripheral nervous common containing a polypeptide or polynucleotide system, such as peripheral nervous injuries, peripheral nervous common containing a polypeptide or polynucleotide contained and central nervous system disease, such as Cativing the activity or property containing containing a polypeptide containing containing a polypeptide containing a polypeptide or polynucleotide or polynucleotide containing a polypeptide or polynucleotide containing a polypeptide or polynucleotide or polynucleotide or polynucleotide or polynucleotide or polynucleotide or polynucleotide or polypeptide or polynucleotide or polypeptide or polypeptide or polynucleotide or polypeptide or polypeptide or polypeptide or polypeptide
Sequence 1066 BP; 225 A; 348 C; 325 G; 168 T; 0 other;
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Best Local Similarity Matches 746; Conserv Query Match Best Local (413 410 350 293 290 233 230 110 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGG 169 173 170 AGGGGACCCGGCTCCACCACACACACACCGCCCCTAGAGAGCGCAGCCATCTGGAGCA AGGGGACCCGGCTCCACCACACACACGCGCCCCTAGAGAGCGCAGCCATCTGGAGCA 829 GCCACTACCCGGGGTCCTTCCAGCACCAGCAGCAGCAGTGGGCCGCCCTCCTTGCTGG GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGGAGGAGTGGGCCGCCCCCCTCCTTGCTGG CGTGCTACGGCAGCGGGGGGCGCATGGAGGGGGCCGCCGGCCTACAGCGAGGTCATCG AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACCAGAACCATCTTCGACAGTGACCTGA AGCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG AACTGAACCGGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA GCACAGTGTCAGGCAACGGAATCCCAGAGGCGCAGGTCTACGCCCCGCCTCGGCCACCG GCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA GCCAGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA CGGACGACGATCTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG 172 Conservative 86.2%; Score 742.4; DB 22; 99.2%; Pred. No. 4.6e-143; 0, Mismatches Indels Length 0; 772 769 Gaps 712 709 652 649 592 589 532 472 469 409 352 349 289 292 0

polypeptides, useful for system injuries -

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                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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25-APR-2000;
09-JUL-2000;
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                                                                 Note: The sequence specification.
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                                                                                                                                                                                                                               ABK12142
                                heart
                                                                                                                                  Mouse
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                                                                                                                                                                                                                                                                                                                 AGGATAAACAGAAAGGACACCCTCTC
                                failure.
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0; Mismatches
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RESULT 10
ABK12142
ID ABK122
XX ABK12
XX ABK12
XX O5-JU
DT 05-JU
DY MOUSE
XX MOUSE
XX MOUSE
XW CAITGI
KW C
                                                                                                             Mouse; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arterioscleroscients
    musculus
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                                                                                                                                                                                                                                                                                                                                      CC The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC Cardiac cell anti-apoptotic activity and fragments of it provided CC (MIVA)-1 identical to Genbank sequences AI761441.1, AI594390, CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of CC with a candidate agent, where the molecule is a nucleic acid molecule (CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its CC expression product, determining if the anti-apoptotic activity is CC apoptotic molecules and nucleic acids of the invention are useful for CC treating, diagnosing and monitoring progression of such diseases and CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC encodes mouse MIVR-1.
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                               304
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                                                                                                                                               131
                                                                                                                                                                                                                                                                                                                      Sequence 878 BP; 179 A; 305 C; 247 G; 147 T; 0 other;
                                                                                                                                                                      124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
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                                                                                                                                                                                                                       11 CATGGCTTGATGGGGGTCAACGGCACCGCCGCCGCCGCCGGGCAGCCCAATGTCTCC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 99-100; 105pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee RT,
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AGAGACGATGGACTGTCCTCGGAAGGATGCCTCTGGCCCTCAGAGAGTACGGTGTCAGG-
                                                                                             AGAGAAGATGCCCTCTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGC
                                                                                                                                         GTTCAGATCATCATCATCGTGGTGGTGATGGTGGTGGTGGTGATCACGTGCCTG
                                                                                                                                                                                      TGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTT 123
                                                                                 CTGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACAGCCCAGGCCAGGAGG
                                                                                                                               GTGCAAATCGTGGTCATCGTGGTAGTGATGATGGTGATGGTGGTTATGATTACGTGCCTG
                                                                                                                                                                            TGCGCGTGCAACTGCCAGCGCTCTTTGTTCCCCCAGCATGGAGATCACGGAGCTGGAGTTC
                                                                                                                                                                                                                                                                                    701;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRIGHAM & WOMENS HOSPITAL INC
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                                                                                                                                                                                                                                                                                 Conservative
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/product= "MIVR-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
20..844
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                                                                                                                                                                                                                                                                                         71.1%;
86.5%;
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                                                                                                                                                                                                                                                                      Score 612.4; DB 24; Length Pred. No. 1.9e-116; O; Mismatches 97; Indels
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RESULT 11
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XX Mus &
YX W201
XX W201
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XX W201
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XX W3 W3
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YX W11-M
PR 01-M
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       (MILL-) MILLENNIUM PHARM INC
                                                         01-MAR-2000; 2000WO-US05226
                                                                                                                                                                                                                      TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; cedema; emphysema; chronic bronchitis; bronchial astima; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halzheimer's Disease; cerebral toxoplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                      01-MAR-1999;
                                                                                           08-SEP-2000.
                                                                                                                   Ю200052022-A1.
                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding a murine TANGO 261 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barnes TM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellu
                                                                                                                                                                                                              Disclosure; Page
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                                                                                                                                                                                                                                                                                       human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TM,
                                                                                                                                                                                                                                                                                                                                                                      AAB18464.
                                                                                                                                                                                                                                                               treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA,
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AAA75166-68 encode murine TANGO 261 proteins. The specification als describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhes and cell trafficking and/or migration, modulate cellular interactic

modulate

TANGO also

adhesion,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC modulate the proliferation, differentiation, and/or function of cells
CC that appear in the bone marrow, and leukocytes, treat bone marrow, blood
CC and hematopoietic associated diseases and disorders, atelectasis,
CC asthma and bronchiectasis, intestinal disorders, spleen associated
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC as ischemic heart disease, modulate the proliferation, differentiation,
CC cartilage associated diseases or modulate the proliferation, differentiation,
CC cartilage associated diseases or disorder. They may also be used to
CC hydrocephalus, brain herniations, iatrogenic disease, inflammations,
CC bacterial and viral meningitis, Alzheimer's Disease, cerebral
CC hydrocephalus and encephalitis, and treat hepatic disorders,
CC note: the present sequence does not appear in the specification; it was
CC created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                     349 ATCTGTGCGCGCACCCCTAACCGGACCATCTTCGACAGTGACCTTATAGACAGCACCAT 408
                                                                                                                                                                                                                                                                                                                        543 GTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 GCCGCCCTTCGCCCAGCGGGAGCGCCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1713
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               ACAGAAAGGACACCCTCTC 861
                                                        CCATCACTCGCACATTGCCCCACTGGA---
ACAGAAAGGTCACCCCCTC
                                                                           CCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAA 842
                                                                                                             CTCCTCCTTCCAGCACCAGCAAGTAACGGGCCATCCTCCCTGCTAGAGGGGACCCGGCT
                                                                                                                              GTCCTCCTTCCAGCAGCAGCAGCAGCAGCAGCGGCCGCCTCCTTGCTGGAGGGGACCCGGCT
                                                                                                                                                                                            CGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGG
                                                                                                                                                                                                                                       GCTGGGCGGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAG
                                                                                                                                                                           CGGTGGCGCATGGAGGGCCGCCCCCACTACAGCGAGGTCATTGGCCACTACCCTGG
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83.7%;
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Pred. No. 2.6e-85;
0; Mismatches 84
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AAA75166-68 encode murine TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The CC proteins can be used to treat any von Willebrand factor-associated CC proteins can be used to treat any von Willebrand factor-associated CC and cell trafficking and/or migration, modulate cellular adhesion, modulate cellular adhesion, modulate cellular adhesion, modulate cellular adhesion, of cell trafficking and/or migration, modulate cellular adhesion, CC modulate the proliferation, differentiation, and/or function of cells CC and hematopoietic associated diseases and disorders, such as cancer, CC asthma and bronchiectasis, intestinal disorders, atteat bone marrow, blood CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial CC astima and bronchiectasis, intestinal disorders, spleen associated CC as ischemic heart disease, modulate the proliferation, differentiation, cCC cartilage associated diseases, modulate the proliferation, differentiation, CC cartilage associated diseases or disorder. They may also be used to hydrocephalus, brain herniations, latrogenic disease, inflammations, CCC bacterial and viral meningitis, Alzheimer's Disease, cerebral codema, and treat hepatic diseases, brain cancers, created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barnes TM, Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
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120 302 GCTGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACACCAGCCCAGGCCAGGAG

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Conservative

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CC AAA75166-68 encode murine TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular proliferation. The CC cellular differentiation and/or modulate cellular datesion. The CC proteins can be used to treat any von Willebrand factor-associated CC disorder, regulate extracellular matrix structuring, cellular adhesion, and cellular interactions, cc modulate cell adhesion in proliferation, modulate cellular interactions, cc modulate cell adhesion in proliferative disorders, such as cancer, cc modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cc pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial cc asthma and bronchiectasis, intestinal disorders, spleen associated cd diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, cand/or function of bone and cartilage cells and to treat bone and/or cartilage associated with the ovaries, and corebral bone and/or cartilage associated with the ovaries, and cerebral cedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, cc bacterial and viral meningitis, and treat hepatic disorders. hydrocephalus and encephalitis, and treat hepatic disorders. twas created using information encoursed.
 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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Score 460.6; DB 2
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Human MIVR-1 homologous seq
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Human; ss; MIVR-1; Mechanic
KW cytostatic; cardiant; cereb
KW cardiac cell; anti-apoptoti
KW cardiac cell; anti-apoptoti
KW cardiac hypertrophy; myocar
XX

heart failure; AI761441.1.
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PN W0200216416-A2.
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PPD 28-FEB-2002.
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PPD 28-FEB-2002.
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PPF 21-AUG-2001; 2001WO-US26089
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PFF 21-AUG-2000; 2000US-227159p
PAA (BGHM ) BRIGHAM & WOMENS HO
PAA (PFIZ ) PFIZER INC.
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PPI Lee RT, Landschulz KT, Ke
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PPT Novel nucleic acid molecule
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Novel nucleic acid molecule encoding Mechanically Induced Vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR-1 polypeptide having CC cardiac cell anti-apoptoric activity and fragments of it provided CC they are not identical to Genbank sequences AIT61441.1, AI594390, CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of CC MIVR-1, contacting a molecule having cardiac cell anti-apoptoric activity with a candidate agent, where the molecule is a nucleic acid molecule (CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-1)d or its CC expression product, determining if the anti-apoptoric activity is CC expression product, determining if the anti-apoptoric activity is CC expression decules and nucleic acids of the invention are useful for CC treating, diagnosing and monitoring progression of such diseases and cCC endothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC stroke, arteriosclerosis and heart failure. The present sequence CC is one of the four Genbank sequences (AI761441.1) which are homologous to XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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ACAGAAAGGACACCCTCTC 861
                                           CAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAG
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485; Conservative
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Pred. No. 2.7;
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Search completed: March Job time : 238.388 secs

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Perfect score:
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1: /cgn2_6/ptodata/1,
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-185-246A-5
US-08-485-246A-5
US-09-194-005-7
US-09-146-249A-64
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US-09-128-155-16
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US-09-429-516-2
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US-09-091-952A-6
US-09-091-952A-8
US-07-945-283-1
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US-08-924-440-1
US-08-804-227C-7
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US-08-476-176B-7
US-08-127-721A-7
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4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9
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Sequence 2, Appli	Sequence 1, Appli Sequence 2, Appli		Sequence 78, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl

ALIGNMENTS

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Sequence 7, Applicatio Patent No. 6458532 GENERAL INFORMATION:
                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-OCT-1996

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367

REFERENCE/DOCKET NUMBER: 015280-297100US

TELEDHONE: (415) 576-0300

TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO; for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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LENGTH: 921 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES:
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Yoshikawa, Takeo
Sanders, Alan R.
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Gershon, Elliot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENTIN: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Badner, Judith A. Goldin, Lynn R.
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Sequence 6, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
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OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Best Local Similarity 73.1%;
Matches 482; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CCTGAACAGCAGATGGAACTCAACCGAGAGTCCGTGAGGGCCCCAACCCAACCGAACCATA
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MOLECULE TYPE:
FEATURE:
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LOCATION:
                                                               INVENTION:
                                                                                  Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
                                                 VENTION: Chromosomal Markers and
                                                                                                                                     Gershon, Elliot's,
Badner, Judith A.
Goldin, Lynn R.
                                                                                                                                                           Detera-Wadleigh, So
Gershon, Elliot S.
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cDNA
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                                    Tests for Manic-Depressive
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Pred. No. 1.4e-69;
0; Mismatches 168
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Best Local Similarity
Matches 482; Conserva
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 5595...5685
OTHER INFORMATION: amplified
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
274 CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC
                                               214 TTCATCAGCCGGCACAGCCAGGGGGGGGGGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGC 273
                                                                                                       154 ATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCC
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
                                                                                                                                              281 CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCATCGTCGTGGTGGTC 340
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                               TTCATCAACCGCCCGAACCAGAGCCGGAGGCGGGAGGACGGGCTGCCGCAGGAAGGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-007-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
STATE: CA
COMMENT CACA
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 452...505
OTHER INFORMATION: alternatively spliced portion
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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OTHER INFORMATION: Clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/091,952A FILING DATE: 19-Apr-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                               40.98;
73.18;
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                                                                                                                                                                                                              Score 352.2; DB 4;
Pred. No. 2.3e-69;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                   22 coding region
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RESULT 2 US-09-091-952A-6

APPLICANT:

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RESULT 3
US-09-091-952A-8
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                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                            APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
                                                                                                                                  PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                               STATE: CA
                                                                                                                                APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: Chromosomal Markers and Dia
Tests for Manic-Depressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Detera-Wadleigh, Son Gershon, Elliot S. Badner, Judith A. Goldin, Lynn R.
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Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
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INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                           CCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC 573
                                                                                                                                                                                                                                                    CTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC
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             ACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCAGCAGCAGCAGCAG
                                                                                                                                              TTCGACAGTGACCTGATGGATAGTGCCAGG----CTGGGCGGCCCCCTGCCCCCCCCCAGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCATCAGCCGGCACAGGCCAGGGGGGAGGAGAGATGCCCTGTCCTCAGAAGGATGC 273
                                                       AACTCGGGCATCAGTGCAAGCACCTGCAGCAGTAACGGGAGGATGGAGGGGCCACCCCCC
                                                                                     AACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCGCATGGAGGGGCCGCCGCCC
                                                                                                                  CTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCTGCACCCTGCAGCTCCGGGAC
                                                                                                                                                                                                                                                                                               CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC
ACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAGCGCAG
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LOCATION: 1...867
OTHER INFORMATION:
spliced coding regic
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TELEFAX: (415) 576-0300
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68.7%;
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Pred. No. 1.6e-54;
0; Mismatches 143;
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RESULT 4
US-07-945-283-1/c
; Sequence 1, Application
; Patent No. 5352596

US/07945283

GENERAL INFORMATION:

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                                                                                                                                                                                               US-07-945-283-1
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                   Matches
6121
                                                                                       473 CCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCGGAGCAGCAGCTGGAAC 532
                                                                                  413
                                                                                                           353 GCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATC 412
                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/
ETLING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: 309-685-4128
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE NO
                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL
                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLECULE TYPE:
                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TRM DC COMPUTER
                                                                                                                                                                                                                                                                          OCATION:
                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             COCATION:
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                           CGTACCTGCAGCACGAGATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAGGAGC
                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1815
CITY: Peoria
                                                                                                                                                   189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61604
                                                                                                                                    11arity 46.4%; Score 47.8; DB 1; Length 8438; Conservative 0; Mismatches 217; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8438 base pairs
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replace(7010, "g")
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1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
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Involving The EPO and LLT Genes
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US-08-785-420-1
Query Match
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US-08-785-420-1/c
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                                                                                                                                                                            TELEFAX: 704-334-2014
TELEX: 57-5102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
                                      CLONE: POTCINE I
POSITION IN GENOME:
UNITS: bp
                                                                          ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                TOPOLOGY: 1; MOLECULE TYPE:
                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION: 704-377-1561
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/030,159
FILING DATE: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Layton,JT., Samuel G.
REGISTRATION NUMBER: 22807
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MacLennan, David H
APPLICANT: O'Brien, Peter J.
TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
TITLE OF INVENTION: HYPERTHERMIA
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                          TELEPHONE: 704-334-2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15378 base pairs
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                          Porcine RYR1 Gene
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6001976
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                                                                                                             DNA (genomic)
                                                                                                                                         single
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Drawer 34009
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5.4%;

Score 46.2;

DВ ω,

Length 15378;

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325

GTCTACGCCCCGCCTCGGCCCACCGACCGCCTGCCGTGCCGCCCTTCGCCCAGCGGGAG 384

Matches

Conservative

0;

50.7%;

Pred. No.

ed. No. 0.17; Mismatches 108;

Indels

0;

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Best Local Similarity

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RESULT 6
US-08-476-176B-7
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                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILLING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,80
FILLING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                            TELEFAX: (908) 277-430
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13329 GTCCGCCTCGCCGGCCGGCCCAGCCGGCTGCTCGTCGCCCCTCGTCGCCCCTGGATC 13270
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APPLICANT:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 424 base pairs
                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                   FEATURE:
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                 NAME/KEY:
LOCATION:
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
 OTHER INFORMATION:
                                                                   OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAG 543
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                                                                                                                                                                               424 base pairs
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59 Route 10
                                                                                                                                                                                                                                   (908) 277-4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                CDS
22..402
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Kolbinger, Frank
                 mat_peptide
82..402
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                                                                                                                DNA (genomic)
                                                                                                                                                 double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5958708artis Patent Department
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/product= "light chain variable
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; OTHER INFORMATION: region C21-L2 US-08-476-176B-7
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US-08-127-721A-7
                                                                                                         APPLICATE APPLICATE APPLICATION:
FILING DATE: 25-SEPIECE.
ATTORNEY/ACENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
777-4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08127721A Patent No. 6066718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 136; Conserv
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hardman
                                                                                                     TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kolbinger
APPLICANT: Saldanha,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                   TOPOLOGY:
                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                        CENGTH:
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                                                   nucleic acid
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                                                                       424 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 Route 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                     linear
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DNA (genomic)
                                      double
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                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                          Version
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US-08-485-246A-7
                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER: 1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/1
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GENERAL INFORMATION:
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LOCATION: 82..402
OTHER INFORMATION: /product= "light chain variable US-08-127-721A-7
         TELEPHONE: (908) 277-5110
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relase #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Best Local 9
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APPLICANT:
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 TELEFAX:
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CITY: E
STATE:
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                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07936-1080
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cal Similarity 47.4%;
136; Conservation
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(808)
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Saldanha, Jose
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                                                                                                                                                                                                                                                                                                                                                  Hanover
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22..402
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LOCATION: Mat_peptide
LOCATION: 82..402
OTHER INFORMATION: /prod
OTHER INFORMATION: regio
US-08-485-246A-7
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US-08-924-440-1
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Best Local Similarity 4/...
136; Conservative
                                                                             SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/924,440 PILING DATE: August 27, 1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
TELECOMMUNICATION INFORMATION:
                                                  ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Sto
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
            NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                         OPERATING SYSTEM:
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CITY: Palo Alto
STATE: CA
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47.4%;
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Pred. No. 0.11;
0; Mismatches 151;
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RESULT 10
US-08-804-227C-7
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GENERAL INFORMATION:
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TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 1:
                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x-
                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOSOFTWARE: ASCI(DOS) TECTION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                         TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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STRANDEDNESS: single
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                                                                                                                                                                                                 APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: INDIANAPOLIS
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                                                                                                                                                                                  CLASSIFICATION:
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                       LENGTH:
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: 44377 base pairs
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                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM Compatible
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47.58;
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                                                                                                                                                                                                                                                      Text only
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Pred. No. 0.
                                                                                                              X-8231
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Mismatches 145;
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US-08-804-198-1
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                                                                                                                                                            Sequence 1, Applic Patent No. 5945320
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                                               CORRESPONDENCE ADDRESS:
                                                                        APPLICANT: ROSTECK, Paul R., Jr. TITLE OF INVENTION: PLATENOLIDE
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STATE:
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            INDIANAPOLIS
                                                                                                                                                                         Application US/08804198
                       E: PAUL R. CANTRELL 1138
LILLY CORPORATE CENTER
                                                                                                                      Burgett, Stanley G.
Kuhstoss, Stuart A.
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                                                                                              Rao, Nagaraja R.
Richardson, Mark A.
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Macintosh

Floppy disk

COUNTRY:

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INFORMATION FOR SEQ ID NO:
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LOCATION:
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nucleic acid
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Pred. No. 0.65;
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US-08-476-176B-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                543 GTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAG 602
                                                                                               483 CCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGA 542
                                                                                                                                                                                                          NAME/KEY: mat_peptide LOCATION: 82..402 OTHER INFORMATION: /pi OTHER INFORMATION: reg
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ZIP: 07936-1080
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nucleic acid
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region C21-L1"
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US-08-476-176B-9
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                  Query Match
Best Local S
 Matches
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,80
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    TELEFAX: (908) 277-43
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                            FEATURE:
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                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                           LOCATION:
                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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al Similarity 47.0
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nucleic acid
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NO: 9:
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                                                                             /product= "light chain variable
region C21-L3"
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 Score 43.8; DI
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0; Mismatches
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RESULT 14
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                                                                                                                                                                                                                                                TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hardman, APPLICANT: Kolbinger APPLICANT: Saldanha, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4-TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 277-5110
                                                                      LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEPTEMBE ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: doub
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OPERATING SYSTEM: PC-DOS/MS-DOS
   OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                             TOPOLOGY:
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/product= "light chain region C21-L1"
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ER: 4-19276/A/P2/CIP
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RESULT 15
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PARTING DATE: 27-SEPTEMBER-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA: 07/952,802

PRIOR APPLICATION DATA: 07/952,802

FILING DATE: 25-SEPTEMBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6066718ak, Henry P.

REGISTRATION NUMBER: 33,200

REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP

TELEPHONE: (908) 277-5110

TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08127721A Patent No. 6066718 GENERAL INFORMATION:
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Best Local Similarity 47.0%;
Matches 135; Conservative
                                                                                                                                                                                TELEPHONE: (908) 277-
TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                  FEATURE:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6066718art1s Patent and Trademark Department STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
                                                              MOLECULE TYPE:
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APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
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                           NAME/KEY: CDS
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                                                                                   TOPOLOGY:
                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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ZIP: 07936-1080
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277-4306
277-9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: mat_peptide
; LOCATION: 82..402
; OTHER INFORMATION: /product= "light chain variable
; OTHER INFORMATION: region C21-L3"
US-08-127-721a-9
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Best Local Similarity 47.0%;
Matches 135; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: FEATURE:
                                                                                                                                                                                        603 GCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAG 662
336 GTACTACTGCCAGCAGAGCGACAGCTGGCCCACCACCTTCGGCCAGG 382
                                                  723
                                                                                          276
                                                                                                                    663 CGGCGGGCCATGGAGGGGCCGCCCCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGG 722
                                                                                                                                                              216 GCTGCTGATCAAGTACGCCAGCGAGAGCATCAGCGGCATCCCCAGCAGGTTCAGCGGCAG 275
                                                                                                                                                                                                                                               156 CAGCCAGAGCATCGGCACCAACATCCACTGGTACCAGCAGAAGCCCGGCCAGGCCCCCAG 215
                                                                                                                                                                                                                                                                                     543 GTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAG 602
                                                                                                                                                                                                                                                                                                                                                         483 CCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGA 542
                                                                                                                                                                                                                                                                                                                               96 CCAGAGCCCCGGCACCCTGAGCCTGAGCCCCGGCGAGAGGGCCACCCTGAGCTGCAGGGC 155
                                 GTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG 769
                                                                             CGGCAGCGGCACCGACTTCACCCTGACCATCAGCAGGCTGGAGCCCGAGGACTTCGCCAT 335
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 424;
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Search completed: March 17, 2003, 14:13:23 Job time : 90.4322 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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Result
No.
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Maximum DB seq
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Perfect score:
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       0000 00
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                         861
755.2
742.4
612.4
544.4
462.2
445.6
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      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501302 seqs, 350932545 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      : /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US0_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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                  861
1321
969
1066
878
1713
1713
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8093
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1273
12733
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      US-09-796-753-55

US-10-098-841-71

US-09-934-249-12

US-10-000-256A-32

US-09-796-753-57

US-09-794-249-16

US-09-934-249-15

US-09-934-249-15

US-09-783-590-3464

US-10-152-548-9

US-10-152-548-9

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US-10-032-393-8
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US-09-934-249-1
                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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8233.708 Million cell updates/sec
Sequence 55, Appl
Sequence 71, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 57, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 3464, Ap
Sequence 3468, Ap
Sequence 332, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                      Description
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Sequence
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42.2 42.2 2.2	42. 42. 42. 42. 42. 42. 2	42.8 42.4 42.4 42.2 42.2	42 43 . 22 . 8 8 8 3 . 8	43.8 43.8 43.8	44.6
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18596 18596 18596	1085 2048 2092 2389 18596	4183 4166 4238 464 1074	3705 3705 3705 152331 4826 470 522	735 321 3162 6854 58985	370 465
9 10 10	9 10 10	10	10 10 10	9 10 9	10 10
US-09-954-531-348 US-09-880-107-1590 US-09-967-768A-119	US-10-024-828-3 US-09-925-301-260 US-09-926-841-271 US-09-799-875-7 US-09-954-531-124	US-09-757-716-2 US-09-782-980-73 US-09-796-338A-4 US-09-864-761-764 US-09-864-761-764	US-09-954-531-1023 US-09-880-107-2175 US-10-095-407-16 US-09-772-304A-1 US-09-864-761-3121 US-09-864-761-19900	US-09-991-470-26 US-09-991-470-24 US-09-815-242-4081 US-09-922-683-7 US-09-901-152-3	US-09-728-446-223 US-09-864-761-230
m m	Sequence 3, Appli Sequence 260, App Sequence 271, App Sequence 7, Appli Sequence 124, App	Sequence 2, Appli Sequence 73, Appl Sequence 4, Appli Sequence 764, App Sequence 9, Appli	1 0 4 4 9 9 9	Sequence 26, Appl Sequence 24, Appl Sequence 4081, Ap Sequence 7, Appli Sequence 3, Appli	Sequence 223, App Sequence 230, App

ALIGNMENTS

US-09-934-249-3

Sequence 3, Application US/09934249 Patent No. US20020115081A1

Richard T

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                                                                                                                                                                                                                                                        ; ORGANISM: Homo Sapiens FEATURE: ANAME/KEY: CDS LOCATION: (1)...(861) US-09-934-249-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lee, Ric
APPLICANT: Landsch
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                     Query Match 100.0%; Score 861; DB 10; Best Local Similarity 100.0%; Pred. No. 9.3e-186; Matches 861; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 861
121 TTTGTTCAGATCATCATCGTGGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC
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                                                   TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
                                                                                                                      Turi, Thomas G.
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121

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DB 10; 0;

Indels Length

0,

Gaps

0

472

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RESULT 2
US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS CURRENT APPLICATION UNUMBER: US/09/934,249
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
PRIOR APPLICATION NUMBER: US/09/934,249
PRIOR APPLICATION NUMBER: US/09/934,249
PRIOR APPLICATION NUMBER: US/09/934,249
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1321
                                                                                                                                                                                                                        841 AAACAGAAAGGACACCCTCTC 861
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                                                                                                                                                                                                                                                                                                                                                                                                           CTCCACCACACACACCCCCCCCCCCTAGAGAGCCCAGCCATCTGGAGCAAAGAAGAAGAT
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FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1
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Best Local
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    AAACAGAAAGGACACCCTCTC
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                                  CTCCACCACACACACATGGCGCCCCTAGAGAGGGCGCAGCCATCTGGAGCAAAGAAGAAGGAT
                                                                      473
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                                                                                                            AGCGGCGGGCGCATGGAGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCG
                                                                                                                                                   AGGCTGGGCGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC
                                                                                                                                                                                        61
                                                                                                                                                                                                                                         TACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG
                                                                                                                                                                                                                                                                    CAGCACGAGATCGACCTGCCACCACCACCACCTGTCTAGACGGGGAGGAGCCCCCACCC
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Conservative 0
     1273
                       861
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Pred. No. 1e-185;
Mismatches 0
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US-09-796-753-55

840 1192

1132 720 1072

660

1012 600 952

892 480 832 420

360

652 240 592

780

781 781 721 721 661 661

601 109

221 61 161

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HENGTH: 969
TYPE: DNA
ORGANISM: HOMO SA
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(
US-09-796-753-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-12-3
PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/2
PRIOR PILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/2
PRIOR APPLICATION NUMBER: 09/3
PRIOR APPLICATION NUMBER: 09/312
                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 55
LENGTH: 969
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                                    Query Match
     Best Local Similarity 99.0 Matches 757; Conservative
                                                                                                                                                                                                                                                             PRIOR
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CURRENT FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DR APPLICATION NUMBER: 09/51
DR FILING DATE: 2000-02-25
DR APPLICATION NUMBER: 09/51
DR FILING DATE: 2000-03-01
DR APPLICATION NUMBER: 09/57
DR FILING DATE: 2000-05-14
DR APPLICATION NUMBER: 09/59
DR APPLICATION NUMBER: 09/59
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DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-23
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/47
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R APPLICATION NUMBER: 09/34
DR FILING DATE: 1999-06-30
DR APPLICATION NUMBER: 09/36
DR FILING DATE: 1999-07-30
DR APPLICATION NUMBER: 09/39
DR FILING DATE: 1999-09-20
DR FILING DATE: 1999-09-20
DR FILING DATE: 1999-09-30
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DR FILING DATE: 1999-09-30
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DR FILLING DATE: 2000-07-31
DR FILLING DATE: 2000-06-29
DR FILLING DATE: 2000-06-29
DR APPLICATION NUMBER: 09/60
DR FILLING DATE: 2000-06-29
DR FILLING DATE: 2000-06-29
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FILING DATE: 1999-06-18
APPLICATION NUMBER: 09/
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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ON: SECRETED PROTEINS AND 7853-227-999
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   Score 755.2;
Pred. No. 7.7e
0; Mismatches
   ; DB 9;
7e-162;
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US-10-098-841-71

Sequence 71, Application US/10098841

Publication No. US20020197679A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Ma, Yunqing
APPLICANT: Ma, Yunqing
APPLICANT: Mang, Jian-Rui
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Dunrui
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Zhou, Ping
Ma, Yunging
Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
Wang, Dunrui
Wang, Thiwel
Wehrman, Tom
Zhang, Jie
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; LOCATION: (154)..(867)
US-10-098-841-71
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Best Local S
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770 AGGGGACCCGGCTCCACCACACACACACCGCGCCCTAGAGAGCGCAGCCATCTGGAGCA 829
                                               710 GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGGAGCAGTGGGCCGCCCCCCTTCCTGG
                                                                                    650 CGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG 709
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: PolyPeptides
TITLE OF INVENTION: PolyPeptides
CIPRENT FILE REFERENCE: 784C1P2
CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT APPLICATION NUMBER: US/10/098,841
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                      593
                                                                                                                                                                                                  590
                                                                                                                                                                                                     533 AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 592
                                                                                                                                                                                                                     530 AACTGAACCGGGAGTCGGTGCGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 589
                                                                                                                                                                                                                                                                                                                                    410 ATCCGTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                 470
                                                                                                                                                                                                                                                                                                                        413 ATCCGTACCTGCAGGACGAGATCGACCTGCCACCATCTCGCTGTCAGACGGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                             350 ACCGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT 409
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                               GCCACTACCCGGGGTCCTTCCAGCACCAGCAGGAGGGGCGGCCGCCCTCCTTGCTGG
                                                                                                                                                            TGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCA 649
                                                                                                                                             TegaragreccadecreececececececececadeagraacTceggcatroagcecca 652
                                                                                                                                                                                                                                                            AGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG 529
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99.2%; Pred. No. 6.1e-159;
tive 0; Mismatches 6; Indels 0;
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APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: POT38/T001/ERP/KA
CURRENT APPLICATION UNMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US/09/27,159
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 878
TYPE: NO.
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; LOCATION: (20)...(841)
US-09-934-249-12
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Best Local Similarity 86.5%;
Matches 701; Conservative
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US-09-934-249-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
484 CAGGGCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAG
                                  364 CCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mus Musculus
FEATURE:
                                                                   310 --TGGAATGCCGGAGCCACAGGTCTATGCCCCGCCTCGGCCCACTGACCGACTCGCTGTG
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Pred. No. 1.
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Best Local
                                                                                                                                                                                                                                                                                                                                Matches
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEO ID NOS: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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Local Similarity 99.8%;
les 545; Conservation
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                                                         CCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCC
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Pred. No. 3.6e-114;
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; Sequence 57, Application US/09796753

; Publication No. US20030027998A1
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PRIOR APPLICATION NUMBER: 09/22:
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/25:
PRIOR APPLICATION NUMBER: 60/12:
PRIOR APPLICATION NUMBER: 60/12:
PRIOR APPLICATION NUMBER: 09/31
PRIOR APPLICATION NUMBER: 09/31
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/31
PRIOR APPLICATION NUMBER: 09/31
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/31
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PRIOR APPLICATION NUMBER: 09/34
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/36
PRIOR APPLICATION NUMBER: 09/36
PRIOR APPLICATION NUMBER: 09/39
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PRIOR FILING DATE: 1999-07-30
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RAPPLICATION NUMBER: 09/4
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UMBER: 09/224,246
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CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
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                                                          rthy, Sean A.
DN: SECRETED PROTEINS AND 7853-227-999
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PRIOR FILING DATE: 2000-06-29
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 57
LENGTH: 1713
TYPE: DNA
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US-09-796-753-57
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Best Local S
Matches 569
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              ACAGAAAGGACACCCTCTC
                                                               CCACCACACACACATCGCGCCCCTAGAGAGCGCGCAGCCATCTGGAGCAAAGAAGAAGGATAA 842
                                                                                          CTCCTCCTTCCAGCACCAGCAAAGTAACGGGCCATCCTCCCTGCTAGAGGGGACCCGGCT
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Similarity 83.8%;
69; Conservative
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Pred. No. 1.4e-95;
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RESULT 8 US-09-934-249-14/c

RESULT 9
US-09-34-249-16
; Sequence 16, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:

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APPLICANT: Landschulz, Katherine T.

APPLICANT: Turi, Thomas G.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scott P.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR FILING DATE: 2000-08-22
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Best Local
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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TYPE: DNA
ORGANISM: HOMO S
FEATURE:
    216
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ACAGAAAGGACACCCTCTC 861
                                                                                                                                                                  CCCCCACACACACACCCCTAGAGAGAGCGCAGCCATCTGGAGCAAAGAAGAAGATAA
                                                                     CCACCACACACACACGCCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGATAA
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Pred. No. 6.3e-92;
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NAME/KEY: unsure
; LOCATION: (6837)...(6837)
; OTHER INFORMATION: a or c
US-09-934-249-16
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APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARBLOVASCULAR CONDITIONS FILE REFERENCE: P073B/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934, 249
CURRENT APPLICATION NUMBER: US/09/934, 249
CURRENT APPLICATION NUMBER: US/09/934, 249
PRIOR FILING DATE: 2000-08-22
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Best Local
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APPLICANT:
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ORGANISM: HOMO :
FEATURE:
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SOFTWARE: FastSEQ for Windows Version
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LOCATION: (6477)...(6477)
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TCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAG
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                                                         CAAGCACCTGCAGCAGTAACGGGAGGATGGAGGGCCCACCCCCCCACATACAGCGAGGTGA
                                                                                             CCACGTGCTACGGCAGCGGCGGCGCGCATGGAGGGCCGCCGCCCCACCTACAGCGAGGTCA 706
                                                                                                                                   TAGACATTGCTATGTATAGCGGGGGTCCATGCCCACCCAGCAGCAACTCGGGCATCAGTG
                                                                                                                                                                                                           AACTCAACCGAGAGTCCGTGAGGGCCCCCACCCAACCGAACCATATTTGACAGTGATTTAA
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73.7%;
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Pred. No. 7.1e-70;
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RESULT 11
US-09-783-590-3464
US-09-783-590-3464, Application US/0978; Sequence 3464, Application US/0978; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.

US/09783590

APPLICANT:

646 723 589 663 529 603

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US-09-934-249-15
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
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SOFTWARE: FastSEQ for Windows
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               CACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCC
CACGAAATTGCCCTGCCACCCACCATCTCACTGTCTGATGGGGAGGAGCCCCCCACCC
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                                                           CCCCCCTTCATCCAGCGG---
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85.5%;
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Pred. No. 1.7e-68;
0; Mismatches 57;
                                                        -AGCCGATTCCAACCCACCTACCCCTACCTGCAG
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                                                                          GENERAL INFORMATION:
                                                                                       Sequence 3488, Application US/09783590 Patent No. US20020110850A1
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                         APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
 APPLICANT:
               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 08/420,856 PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 3464
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LOCATION: (367)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (366)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (314)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (279)
OTHER INFORMATION: n equals
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LOCATION: (225)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                835 AAGGATAAACAGAAAGGACACCCTCTC
                                                                                                                                                                                                                                                                    775 ACCCGGCTCCACCACACACACCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAG 834
                                                                                                                                                                                                                                                                                                                  120 AAGGATAAACAGAAAGGACACCCTCTC 146
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 145; Conserv
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Ruben, Steven M.
              Rosen, Craig A.
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98.6%;
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                                                                                                                                                                                                                                                 Prior Application 1
NUMBER OF SEQ ID NO 332
LENGTH: 520
TYPE: PRT
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US-10-184-644-332/c
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                                                                                                                                           Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 332, Application US/10184644 Publication No. US20030044930A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                  ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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NAME/KEY: misc feature
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                                                                          508
     448
                                 528 GGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCT 587
                                                                                                       468 GGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCT 527
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                                                                    GHDDCWSNMAGSW.AS.ACYG.BNH.W..CACTCBMR.TYCMSRC.KYG.B.THSN.W.H 449
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     . ACWACSRRB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard, Audrey
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TYCYNSSCB.YBSBSN.CY.CM.CMBC..CSSCMBC.HCM.CT.C.T
                                                                                                                                         5.3%; Score 46; DB 9; Le 20.2%; Pred. No. 0.11; tive 79; Mismatches 210;
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93.8<del>8</del>;
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Pred. No. 7.
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US-10-152-548-9/c
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                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 CM.CT.C.SC..CMBCT.C.BCS.CMYC..C..CAHCMSCM.CATC.SC.SC..CTYC.S
                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 8600-0167.:

TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Wnt Receptor Compositions and Methods NUMBER OF SEQUENCES: 18
TOPOLOGY: linear MOLECULE TYPE: mRNA
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/152,548 FILING DATE: 21-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250
                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                              TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                       LENGTH: 2334 base pairs
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                                                                                                                                                                                                   Best Local Similarity 48. Matches 127; Conservative
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 2310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09476242 Patent No. US20020146683A1
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BARNETT, Susan
APPLICANT: HARROG, Karin
APPLICANT: MARTIN, Eric
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                  568 ACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 CCGCCCTCCTTGCTGGAGGGGACC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            694 TACAGCGAGGTCATCGGCCACTACCCGGGGTCCTTCCCAGCAGCAGCAGAGCAGTGGG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 CTGTCAGACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 513
                                 688 CCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGC
                                                                                                                                 316 ATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCCCGGCGCCCTGCCCCAAG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 150; Conserv
TGCAACGACAAGAAGTTCAACGGCAGCGCCCCTGCACCAACGTGAGCACCGTGCAGTGC
                                                                                       AGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGGCGCATGGAGGGGCCCCCCG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACC 693
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                                                                                                                                                                                                                                                                                    Description of Artificial Sequence: Vall20-Ala204
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46.3%;
                                                                                                                                                                                                                 48.3%;
                                                                                                                                                                                                Score 45.4; DI
Pred. No. 0.21;
0; Mismatches
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Pred. No. 0.19
0; Mismatches
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.19;
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                                                                                                                                                                                                   136;
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rch cor time	556	808	496	748
Search completed: March 17, 2003, 18:33:25 Job time : 77:3941 secs	556 GAGGGCTGGTGATCCGCAGCGA 578	808 GAGAGCGCAGCCATCTTGCACCAA	496 ACCCACGCCATCCGCCCCTCCACCACACACACACACACCCCCTA 807	AGTGGGCCGCCCTCCTTTCCTTCCTCCTCCTTCCTTCCTT

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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861
1 atgcaccgcttgatgggggt.....aacagaaaggacaccctctc 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16154066 seqs, 8097743376 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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667.4	678.6	700	743.6	792.8	811.8	Score		
77.5	78.8	81.3	86.4	92.1	94.3	Match	Query	d
916	805	1046	967	949	1007	e Match Length DB ID		
14	9	14	14	9	9	DB		
14 BQ954555	AL558881	BM922276	BQ641849	AL517150	AL578575	IB		
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360.8 359.4 358.8	366.2 365.6	369.6 369	375.6 374	388	392	392.2	400	401.6	403	415.2 411	428.2	428.8	430	438.6	445.4	445.4	445.6	461	468	501.6		529.8	550				607.4		
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9 9 14	12 12	10 12	12 14	13	12	12	1 1	12	10	10	<u>, 11</u>	10				14	9	13	12		14	13	13	14	14	11	14	11	9
AA027926 AI972096 BQ575582	BG088400 BG075859	AW071693 BE855409	BF161499 BQ686793	BM482193	BF026695	BG675643	BM974296	BF036086	BE666930	BE553323	BI853324	BB624904	BI156703	AL543170	BQ691500	BQ691705	AI761441	BI646175	BG323347	BM0 / / 002	BQ575741	BI851941	BM141979	BQ015170	BQ690750	AK008976	BQ636742	BC023092	AL558882
€N	BG088400 H3152F10- BG075859 H3152F10-	AW071693 ws53c08.x BE855409 7g13f05.x		~) (J		BM974296 UI-CF-EC1		150581	BE553323 ur44h02.v	BI853324 603379903			Þ			٤		BG323347 602421734	226660 CT-E-EC	ļ		_	_	AGE	σ	2 hd13h06	23092 Mus mu	AL558882 AL558882

ALIGNMENTS

	source	SEATIBEC		COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 AL578575/c
/organism="Homo sapiens" /db_xref="taxon:9606" /clone="cSODK001YC24" /clone_lib="LTI_NFL006_PL2" /tlssue_type="placenta" /note="Vector: pCMV5FORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end	11007	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France	Contact: Genoscope	Unpublished (2001)	Full-length cDNA libraries and normalization	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	1 (bases 1 to 1007)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human .	EST.	AL578575.1 GI:12942781	AL578575	prime, mRNA sequence.	LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D	AL578575 1007 bp mRNA linear EST 16-FEB-2001	

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ORIGIN
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                    CACACACACATGGCGCCCCTAGAGAGGGCGCAGCCATCTGGAGCAAAGAAGAAGAAGATAAACAG
AAAGGACACCCTCTC
           MACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAG
                                                          TCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCTTGCTGGAGGGGACCCGGCTCCAC
                                                                                       TCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCAC
                                                                                                                                                                    GTGCGCGCACCCCCAAACAGAACCATCTTCAACAGTGACCTGATGGATAGTGCCAGGCTG
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                                                                                                                                                                                                                                                                                       CCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCAC 426
                                                                                                                                                                                                                                                                                                                              GGAATCCCAGAGCCGCA-GTCTACGCCCCGCCCTCGGCCCACCGACCGCCTGGCCGTGCCG
                                                                                                                                                                                                                                                                                                                                          GAAGATGCCCTCTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCCGGAGAGCACAGTGTCAGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCBVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://fulllength.invitrogen.com"
293 c 344 g 200 t 10
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Pred. No. 2e-165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 others
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AUTHORS
TITLE
JOURNAL
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ORGANISM
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VERSION
KEYWORDS
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AL517150/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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Best Local
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CCACCGACCGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGC
                                              CGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGC
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                                                                                                             GGCACAGCCAGGGGGGGGGGGGAGGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCT
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Contact: Genoscope
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1 (bases 1 to 949)
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AL517150.1 GI:12780643
EST.
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AL517150 LTI_NFL011_NBC1
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                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fulllength.invitrogen.com"

289 c 330 g 183 t 2 others
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seqref@genoscope.cns.fr, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="CSODA008YB23"
/clone_lib="LTI_NFL011_NBC1"
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Eutheria; Primates;
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98.8%;
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Pred. No. 2.6e
1; Mismatches
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                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 967)
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/clone="IMAGE:6292265"

/clone_lib="NIH_MGC_43"

/clone_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling H
                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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GAGAAGGATAAACAGAAAGGACACCCTCTC
           GAGAAGGATAAACAGAAAGGACACCCTCTC
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99.5%;
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Pred. No. 1.1e-150;
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Plate: LLAM12791 row: n column: 06
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1 (bases 1 to 1046)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
furtrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
205 a 391 c 298 g 150 t 2 others
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/db_xref="taxon:9606"
/clone="TMAGE:5754437"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
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Pred. No. 3e-141;
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BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           Conservative
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segref@genoscope.cns.fr, u
Location/Qualifiers
                                                         Email: fliang@llrerecur.com.
http://fulllength.invitrogen.com"
a 248 c 289 g 161 t
                                                                                        /tissue_Type="T cells from T cell leukemia"
/note="Yector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
Life Technologies, Contact: Feng Lifer Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
http://filliangelifetech.com URL:
                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODJ015YF12"
/clone_1ib="LTI_NFL008_TC2"
                                                                                                                                                                                                                                            /sex="male"
                      78.8%;
99.4%;
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          0;
    Score 678.6; DB 9;
Pred. No. 1.2e-136;
0; Mismatches 4;
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177 GTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGG

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REFERENCE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13626 row: c column: 10
                                                                                                                                                                                                                         BQ954555
BQ954555.1
                                                                                                                                                                                                                                            BQ954555 916 bp mRNA AGENCOURT_8825282 Lupski_sciatic_nerve Homo IMAGE:6204609 5', mRNA sequence.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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  AAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGGCATCAGCCGCCACGTGCTACG
                         -AGGCTGGGCGGCCCTGCCCCCCAGCAGTAACTCGGGCATCAG-CGCCACGTGCTACG
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//dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_2: Sali, cDNA made by Oilgo-dT priming.
/note: Vector: pCMV-SPORT6 (Life Technologies); Sali, cDNA made by Oilgo-dT priming.
/note: Sali, cDNA made by Oilgo-dT priming
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/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/clone=Lib="Lupski_sciatic_nerve"
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            GTCAGGCAACGGAATCCCAGAGCCGCA-GTCTACGCCCCGCCTCGGCCCACCGACCGCCT 179
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Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genos
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/tissue_type="T cells from T cell leukemia"
/note="Twector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Twector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
cloned indo the NotI and Eco RV sides with NotI and
cloned into the NotI and Eco RV sites of the pcMvSpORT 6
Life Technologies Contact: Feng Lidang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
http://filliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                            http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C50DJ015YF12"
/clone_lib="LTI_NFL008_TC2"
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Catarrhini; Hominidae;
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                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 36 Row: h Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                       Center code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, 9
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATAAACAGAAAGGACACCCTCTC
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consorttum (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@man+ Gilbert Smith, Ph.D.
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                                                                                                                                                                                                                                                                                                                                 Submitted (04-FBB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCAGCGGCGGGCGTGGAGGGGGCCGCCGCCTACAGCGAGGTCATCGGCCACTA 539
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/tissue_type="Mammary tumor metastatized to lung.
arose spontaneously from a senescent normal mamman
(clonal) outgrowth infected with the virus MMTV."
/clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
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341 c 289 g 178 t
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/map="CZECH II"
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hd13h06 y1 Human Retina
~~niens cDNA clone
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Mammalia; E
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Plate: 13 row: h column:
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Fax: 301 496 0078
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primer: M13RP1 reverse primer
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                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye dissease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-ppAcTAGTTCTNAATGCGGGCGCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Sumi,N., Ishi,Y., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikagami,T., Kashiwagi,R., Fujiwake,S., Inoue,K., Togawa,Y., Tzawa,M., Ohara,E., Watshiwagi,R., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tzawa,M., Ohara,E., Watshiki,M., Okazaki,Y., Muramatsu,M., Inoue,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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RS Adachi, J. Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, M., Hill, D., Hiramoto, K., Hiracka, T., Hori, F., Karai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sosaba, Y., Suzuki, H., Tagami, M., Sano, H., Sasaki, D., Sosaba, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yoshida, K., Yoshino, M., Muramatsu, M., and
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                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Pax:81-45-503-9216)
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/tissue_type="stomach"
/clone_lib="RIKEN full-length enriched
                                                                                                     /organism="Nus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2210418102"
/db_xref="MGD:MGT:1902457"
                                                         /clone="2210418I02"
/sex="male"
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CTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGC
                                                                                                                                                                                  TCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGG
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                 TCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTC 783
                                                      GGCGGGCGCATGGAGGGGCCGCCCCCCCCCCCCCCACTACAGCGAGGTCATCGGCCCACTACCCGGGG 723
                                                                                                          CTGGGGGGCCCCTGTCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACCTGCTACAGCAGC
                                                                                                                                                                  TCTGTGCGCGCACCCCTAACCGGACCATCTTCGACAGTGACCTTATAGACAGCACCATG
                                                                                                                                                                                                                           CAGGGCCCCTGCACCCTCCAGCTACGGGACCCTGAGCAACAGCTGGAGCTGAACCGGGAA
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VRAPPNRTIFDSDLIDSTMLGGPCPPSSNSGISATCYSGGGRWEGPPPTYSEVIGHYP
GSSFQHQOSNGPSSLLGGTRLHHSHIAPLENKEKGXGHPL"
gSSFGHQOSNGPSSLLGGTRLHHSHIAPLENKEKGXGHPL"
gSSFGHQOSNGPSSLLGGTRLHHSHIAPLENKEKGXGHPL"
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391. .1173
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data source:MGD, source key:MGI:1929600, evidence:ISS
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85.2%;
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TITLE
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nes 615; Conserv
AGGATGCCTGTGGCCCTCGGAGAGCCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGT
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                                                                                 ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGGGAGGAGAAGATGCCCTGTCCTCAGA
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                                                             ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGA
                                                                                                                                      GGTGATGATGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC
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AGENCOURT 8046394 NIH_MGC_110
5', mRNA SEQUENCE
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Tissue Procurement: ATCC
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National Institutes of Health,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/lab_host="Dul08 (phage-resistant)"
/lab_host="Dul08 (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6209341"
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                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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1 (bases 1 to 792)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                  /organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:5834635"
/clone=lib="NGI_GAP_EDI"
/clone_lib="NGI_GAP_EDI"
/clone_lib="NGI_GAP_EDI"
/clone_lib="NGI_GAP_EDI"
/clone_lib="RGI_GAP_EDI"
/clone_lib="RGI_GAP_EDI"
/tlssue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="PHIOB (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT773-Pac
/pharmacia with a modified polylinker; Site_1: Ecor I;
/containing with a modified polylinker; Site_1: Ecor I;
/containing the following tissue(s): Chondrosarcoma cell
/line CS5. The library was constructed according to Bonaldo
/ Lennon and Soares, Genome Research, 6:791-806, 1996.
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
                                                                                                        BM141979
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                                                                                       human.
                                                                                                                                              BM141979 551 bp mRNA linear EST 12-MAR-200 if25a11.yl melton Normalized Human Islet 4 N4-HLS 1 Homo saplens cDNA clone IMAGE:5677341 5' similar to TR:Q9UJD3 Q9UJD3 DJ718J7.1
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Query Match
Best Local Similarity
             826 AGCAAAGAAGAAGGATAAACAGAAAGGACACCCTCTC
                                                                                                    526 CTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCCAAACAGAACCCATCTTCGACAGTGAC
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AGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTC
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                                              CTGGAGGGGACCCGCTCCACCACACACACACCGCCCCTAGAGAGGGCGCAGCCATCTGG
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TAG_LIB-UI-H_ED1

TAG_LIB-UI-H_ED1

TAG_LIB-UI-H_ED1
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TAG_SEQ=CGTCAAGGCT"
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Pred. No. 8.7e-113;
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                   AGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA 601
                                                                                                                                                                                                                                                                                                                                         AGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA
                                                                                    ACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGG
                                                                                                       ACCAGGGCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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617-495-8557
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a 218
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by hydroxyapatite chromatography and used to make this
library.
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/clone_lib="Melton Normalized Human
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/db_xref="taxon:9606"
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TCCACCACACACACGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATA 841
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                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11997 row: h column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BI851941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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                                                                           Similarity
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                                                                                                                                       203
                                                            Conservative
                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 298 c 251 g 142 t
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                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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/strain="FVB/N-3"
/db_xref="taxon:1000"
/clone="IMAGE:5391408"
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                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 729)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, ph.D.
Email: cgapbs-r@mail.nih.gov
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TAG_TISSUE=grade-2-chondrosarcoma
TAG_SEC-ATCTAATATG"
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/clone_lib="NCI_CGAP_Ch2"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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Search completed: March 17, 2003, 13:40:16 Job time : 1621.04 secs

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SUMMARIES

AUTHORS TITLE	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 1 AX392417 LOCUS DEFINITION		.	c 43	4.4	40 40	38	, ω	c 34	ωu) C	o No i	87	თ Մ	24 2		20 3	19 18	16 3 17	1 UI #	13 4	11 12	01			, v,	د <u>م</u> 8	2	Result No. S
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Rae, F. K., Hooper, J.D., Nicol, D.L. and Clements, J.A. Characterization of a novel gene, STAG1/PMEPA1, upre renal cell carcinoma and other solid tumors
Mol. Carcinog. 32 (1), 44-53 (2001)
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                                                               GGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCC
                                                                                         CCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTC
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                                       GGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCC
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YGSGGRNEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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/codon_start=1
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BC015918.1 GI
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hisiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                  BC Cancer Agency, V
                                                                                                                                                                                 CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. CO DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1061)
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                                                                                                                                                 BC Cancer Agency, Vancouver, info@bcgsc.bc.ca
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clone MGC:20374 II
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The I.M.A.G.E. Consortium
                                                                                                                                                                  BC, Canada
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Clone distribution: MGC clone distribut through the I.M.A.G.E. Consortium/LLNL

MGC clone distribution

information can be http://image.llnl.g

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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                GCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCG 792
                                                                                                                                                                                                                                        CTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCC
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                                      AAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGCCCCTGCCC
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nilarity 99.9%;
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protein_id="AAH15918.1"

protein_id="AAH15918.1"

protein_id="AAH15918.1"

protein_id="AAH15918.1"

/db_xref="GI:16198475"

/db_xref="GI:16198475"

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SESTYSGNGIPEPQVIALDEDEQOLELNESVRAPPNRTIFDSDLMDSARLGGPCPPSS
SDGEBEPPPYGGFCTLQLEDPEQOLELNESVRAPPNRTIFDSDLMDSARLGGPCPPSS
SDGEBEPPPYGGFCTLQLEDPEQOLELNESVRAPPNRTIFDSDLMDSARLGGPCPPSS
NGGISATCYGSGGRMEGEPPTYSEVIGHYPGSSFQHQOSSGPPSLLEGTRLHHTHIAP
LESAAIWSKEKDKOKGHPL"

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131. 844
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pred. No. 4.5e-115;
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                                                                             TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG 532
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Mammalia; |
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Patent: WO 0216416-A 3 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, I
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/translation="MHRIMGVNSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQI
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/YGSGGRMEGPPTTYSEVIGHYPGSSFQHQQSGGPPSLLEGTRLHHTHIAPLESAAIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata;
Eutheria; Primates;
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/protein_id="CAD29006.1"
/db_xref="GI:19700735"
                                                                                                                                                                                                                                                                                                             /note="unnamed protein product"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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from Patent WO0216416.
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pred. No. 2.3e-111;
0; Mismatches 0;
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                                                                                                                    XI,L.T. Shanmugam,N., Segawa,T., Sestern Moul,J.W. and Srivastava,S.
A novel androgen-regulated gene, PMEPA1, 20q13 exhibits high level expression in Edenomics 66 (3), 257-263 (2000)
                                                                                                                                                                                                                                               Homo sapiens PMEPA1 protein (PMEPA1) mRNA, AF224278
AF224278.1 GI:9255808
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                                                      Xu,L.L., Shanmugam,N., Somoul,J.W. and Srivastava, Direct Submission
                                                                                                                                                                                                                   Homo
                                          Submitted (12-JAN-2000) CPDR,
                                  Rockville, MD 20852,
                                                                                        (bases 1 to 1141)
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(bases 1 to 1141)
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Location/Qualifiers
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/cell_line="LNCap"
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/chromosome="20"
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                         GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Wilson, J.K.V., Lu, S., Nosrati, A., Swinler, S., Lutterbaugh, J.D., Willis, J., Platzer, P. and Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Mammalia; |
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305 c 247 g 147 t
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Rae,F.K., Hooper,J.D., Nicol,D.L.
Direct Submission
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Rae, F. K., Hooper, J. D., Nicol, D. L. and Clements, J. A. Identification and characterization of a novel gene, up-regulated in renal cell carcinoma and other solid
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                                                                                                                                                                                                                                                                                           where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
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  regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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                                                                                                                                                                 This sequence is the entire insert of clone RP4-718J7 The true end of clone RP5-1007E6 is at 71437 in this sequence. The true right end of clone RP4-579F20 is at 43945 in this sequence. RP4-718J7 is from the library RPCI-4 constructed by the group o Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                               VECTOR: PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 5, 2000 this sequence version replaced gi:10198628.
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HUMAN DNA sequence from clone RP4-718J7 on chromosome 20q13.31-13.33 Contains the PCK1 gene for soluble phosphoenolpyruvate carboxykinase 1, part of a novel gene similar to mouse DLM-1 (tumour stroma and activated macrophage protein), the 3' end of the TMEPAI gene encoding an androgen induced 1b transmembrane protein (PMEPAI), two putative novel genes, a CpG island, ESTs, STSs and GSSs, complete sequence.
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phosphoenolpyruvate carboxykinase; PMEPA1; TMEPAI; transmembrane
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                                                                                                                           was finished as follows unless otherwise noted: all
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1358. 2757
/note="28 copies 50 mer 54% conserved"
1675. .2718
/note="18 copies 58 mer 55% conserved"
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/note="IlMB4 repeat: matches 6088. .6136 of consensus"
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                                 Aluub repeat: matches 1.
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7671
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.2497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copies 55 mer 60% conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copies 4 mer gcac 61% conserved
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               matches 2647.
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15021. .1
                                                                                                                   /note="Aluy repeat: 27603. .27684
                                                                                                                                             /note="16 copies 2 mer tc 87% 26333. .26643
                                                                                                                                                                                                                                  21667. .21775
/note="MIR repeat:
                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ776209" complement(21278. .21663) /note="match: GSS: Em:AQ136459" complement(21392. .21672)
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             /note="L1MB5 repeat: matches 6015. .6176 of consensus" 32224. .32522
                                       /note="FLAM_C repeat: 31203, 31366
                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 90..143 complement(21005..21672) /note="match: GSS: Em:AQ748384" complement(21187...21672)
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15026. .15109
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                                                                                          /note="L2 repeat: matches 2661.
27823. .28041
                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 72.
20413. .20463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 86. .211 of consensus"
18312. .18438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="20 copies 4 mer acac 83% 15273. .15399
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14313. .14437
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13585. .13716
                                                                                                                                                                          25580.
                                                                                                                                                                                                   24257
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18585. .18776
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15029. .15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LTR16C repeat: matches 257.
15015. .15110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="66 copies 2 mer tc 68% conserved"
13588. .13715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="22 copies 6 mer ctctct 67% conserved"
13586. .13717
/note-"AluSx repeat: matches 1.
                                                                            note="MIR repeat: matches 38. .242 of consensus"
                                                                                                                                                                                   /note="L2 repeat: matches 2336. .2710 of
                                                                                                                                                                                                               /note="2
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Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7007305.
During sequence assembly data is compared from overlapping clon
                                                                                                                                                                                                                                                                         150224 bp DNA linear PRI 24-FEE Human DNA sequence from clone RP5-1059L7 on chromosome 20q13.2-13.33 Contains the 5' end of the TMEPAI (PMEPAI) gene encoding an androgen induced 1b transmembrane protein, ESTs, 5
                                                                                                                                                                                                               HTG;
                                                                                         Direct Submission
                                                                                                           Skuce,C
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Mammalia;
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AL121913
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Pred. No. 1.9e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP5-1059L7 The true This sequence is the entire insert of clone RP5-1059L7 The true left end of clone RP11-402F1 is at 106677 in this sequence. This sequence was finished as follows unless otherwise noted: all sequence was finished as follows unless otherwise noted: all trenate regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1059L7 is from the library RPCI-5 constructed by the group of Pieter de Jong. For first-ther Jacks 11 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20 constructed by the Sanger Centre Chromosome 20 constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/chr20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: PCYPAC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="dJ105917.1.2 (androgen induced type 1b
transmembrane protein (PMEPA1), isoform 2)"
/protein_id="CAC32857.1"
/db_xref="GI:13150408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental complement(join(<2445. .2599,53362. .53365)) /gene="TWEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein (PMEPA1),
/note="match: cDNAs: Em:AF224278
match: ESTs: Em:AA088767"
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/note="L2 repeat: matches 2616.
complement(2445. .53425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 46. .165 of consensus" 2076. .2155
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/clone="RP5-1059L7"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 71. .145 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="dJ1059L7.1.2 (androgen induced type transmembrane protein (PMEPA1), isoform 2)"
                                                                                                                                                                                                                            /product="dJ1059L7.1.1 (androgen induced type 1b transmembrane protein (PMEPA1), isoform 1)"
/note="match: cDNAs: Em:AF009426 Em:AF009427 Em:AF009425
                                                                                                                                                                                                                                                                                                                                                           complement(join(<2445. .2599,52376. .52477))
                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="continues in dJ718J7 (AL035541)"
                     complement(join(<2445. .2599,52376. .52472))
/gene="TMEPAI"
                                                                                                                                                                                                    Em: AF009424
/note="continues in dJ718J7 (AL035541)
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                                                                                                                                                             ESTS: Em:AA249792 Em:AI594390 Em:AA128075
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353. 3932
/note="10 crr
3573.
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4792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein (PMEPA1),
/protein_id="CAB88144.1"
/db_xref="GI:7619746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-not_experimental
/product="dJ1059L7.1.1 (and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="3 cc-
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                                                                                                                                                                                                                                                                                                                                                                    /note-"MIR repeat: matches 48. .161 of consensus complement (8858. .9277)
                                                                                                                                                                                                                                                                                                                                                                                                                                      5002. .5190
/note="MER20 repeat: matches 1.
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/note="MIR_repeat: matches 94. .154 of consensus"
                                                                                                                                                                                                                                                                                                                                                        /gene="TMEPAI"
                                                                                                                                                                                         /note="MIR repeat: matches 11. .196 of consensus"
11630. .12037
                                                                                                                                                                                                                               note-"Charlie4 repeat: matches 39. .146 of consensus"
                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ757992"
                                                                                                                                                                                                                                                                                      9286. .9706
/note="match: GSS: Em:AQ565377"
                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 81. .239
                                                                                                                                                                                                                                                                                                                                          'note="match: GSS: Em:AQ881699"
           /note="MIR repeat: matches 7 ..254 of consensus"
16989 ..17387
                                                                                                            14634. .14813
                                                                                                                         14448. .14493
/note="23 copies 2 mer at 76% conserved"
                                                                                                                                                /note="AluSx repeat: matches 1. .311 of consensus"
                                                                                                                                                                            /note="L2 repeat: matches 2290.
                                       /evidence=not_experimental
15690 .15935
                                                                                 /note="MER20 repeat:
15096. .15497
                                                                'note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ="3 copies 37 mer 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copies 2 mer tt 81% conserved"
repeat: matches 1. .374 of consensus
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in (pMEPA1), isoform 1)"
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repeat_region

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Matches
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Best Local
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                                                                                                                       CGGCGGCGGCGGCGGCGGCGCTCGGCTGGGGAAAGCTAGCCGCCAGAGGCTCAGCCCC 120
GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAG
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                                  CTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGGCAGCCCAATGTCTCCTGCAC
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17699. .18179
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/note="18 copies 2
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26450. .26485
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24460. .24580
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23439. .23512
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20530. .21282
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20264. .20432
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19954. .20005
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17902. .18039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MD1 repeat: matches 6102. .6221 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1MD2 repeat: matches 5595.
                                                                                                                                                                                                                                                                                                                                                                                                            39.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                Score 522.8;
Pred. No. 1.9e
0; Mismatches
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AX392430
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Eukaryota; M
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
GAACTGAACCGGGAGTCGGGGCACCCCCAAACAGAACCATCTTCGACAGTGACCTG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone_lib="Novagen Cat. No. 6
/dev_stage="16 day embryo"
<1. .609
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/product="Nedd42471"
/protein_id="AaG442471"
/db_xref="Gi:12004974"
/translation="SQARRRDDGLSSEGCLWPSESTVSGGMPEPQVXAPPRPTDRLAV
/translation="SQARRRDDGLSSEGCLWPSESTVSGGMPEPQVXAPPRPTDRLAV
ppFIQRSREQPTYPYLOHEIALPPTISLSDGEEPPPYGGPCTLOLDDPEQQLEILNRES
vRAPPNRTIFDSDLIDSTMLGGCPPPSSNSGISATCYSSGGRWEGPPPTYSEVIGHYP
GSSFQHQOSNGPSSLLEGTRLHHSHIAPLENKEKEKOKGHPL"
gSSFQHQOSNGPSSLLEGTRLHHSHIAPLENKEKEKOKGHPL"
gSSFQHQOSNGPSSLLEGTRLHHSHIAPLENKEKEKOKGHPL"
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Pred. No. 2.4e-50;
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Adelaide, SA 5000, Australia
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                                                     AAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATC 550
                                                                                                                           AGTOTTACGCCCCCCCCCCCCACCGACCGCCTGGCCGTGCGCCCCTTCGCCCAGCGGAG
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Sequence
AX011709
                                                                                        GTCAACAGCACCGCCGCCGCCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGC
                                  ATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAG 610
ATCGTGGTGG---
                                                                                                                                                                                                                                                                                                                           Human nucleic acid sequences obtained from pancreas Patent: WO 9955858-A 107 04-NOV-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER (DE); PILARSKY CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 812)
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107 from Patent WO9955858.
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272 c 237 g
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77.4%;
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Pred. No. 2.3e-49;
0; Mismatches 122;
                       TCACGTGCCTGCTGAGCCACTACAAG
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Sequence 1739 from Patent WO0102568
AX071267
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                                                                                                                                                                                                                                                                                                                                                                                                  Human genes and gene expression products Patent: WO 0102568-A 1739 11-7AN-2001; CHIRON CORPORATION (US), HYSEQ, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/db_xref="taxon:9606"
159 c 115 g 5
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941 GAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCA 983
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Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 155649 bases at least Q40
Consensus quality: 155746 bases at least Q30
Consensus quality: 155743 bases at least Q20
Insert size: 155775; sum-of-contigs
Insert size: 162242; 2.6% error; agarose-fp
Quality coverage: 7.64x in Q20 bases; sum-of-contigs Quality
coverage: 7.40x in Q20 bases; agarose-fp
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 156075)
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/note="assembly_fragment:00303
fragment_chain:1"
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/chromosome="2"
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Qy 844 CGACCTGCCACCACCATCTCGCTGTCAGACGGGAGGAGGACCCCACCCTACCAGGGCCC 903
Db 134599 TGCCCTGCCACCCACCATCTCACTGTCTGATGGGGAGGAGCCCCCACCCTACCAGGGCCC 134540
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Search completed: March 17, 2003, 15:52:39 Job time: 4330.22 secs
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fragment_chain:1"
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/note="assembly_fragment:01393
fragment_chain:1"
96059. .156075
/note="assembly_fragment:01880
fragment_chain:1"
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Listing first 45 summaries
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Human polynucleoti
Human polynucleoti
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DNA encoding human

ALIGNMENTS

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RESULT 1
ABK12137
ID ABK1
Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac typertrophy; myocardial infarction; stroke; arterioscleros
        22-AUG-2000; 2000US-227159P
                                                                                                                                                                                                                                                                                               05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                        ABK12137;
                                21-AUG-2001; 2001WO-US26089
                                                                               WO200216416-A2
                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                       Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
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                                                                                                                                         Location/Qualifiers 413..1276
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/product= "MIVR-1"
/note= "This region is specifically claimed in claim
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Best Local Similarity
Matches 1321; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; 440
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1321; DB 24;
Pred. No. 1.2e-203;
; Mismatches 0;
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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; cedema; emphysema; chronic bronchitis; bronchial asthma; bronchiecta; intestinal disorder; spleen associated disease; renal disorder;
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                                                      266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
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congestion; bronchiectasis;

cardiovascular disorder; ischemic heart disease;

hydrocephalus;

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                                                                                                                                                              cellular adhesion. The proteins can be used to treat any von Willebrand C factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative (cellular interactions, modulate cell adhesion in proliferative (cellular interactions, modulate the proliferation, differentiation, cand/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and collection of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and collection of cells that asthma and bronchiectasis, intestinal collections, bronchial asthma and bronchiectasis, intestinal collections, puleon associated disease, modulate renal disorders, treat collections, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or cells and to treat bone and/or cartilage associated diseases or covaries, cerebral cedema, hydrocephalus, brain herniations, iatrogenic collections, bacterial and viral meningitis, Alzheimer's collections, bacterial and viral meningitis, Mizheimer's parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
                                                                                                     Query Match
Best Local S
Matches 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel
262, 3
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Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000;
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                  574
                                                          514 GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGATGATGGTGAT 573
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GGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG
                                           GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of cellular processes, for treating cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB18449.
                                                                                                                  Similarity
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                                                                                                     Conservative
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                                                                                                                                                            вP;
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90..764
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6..89
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99.6%;
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                                                                                                   Score 803.2;
Pred. No. 1.5e
0; Mismatches
                                                                                                   0;
                                                                                                                                                           294 G;
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                                                                                                                                                            148 T; 0 other;
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s, and treat hepatic
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                                                                    WO200230268-A2
                                                                                              Mammalia
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                                                                                                                                                                                                                                                                                                                                 CTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCCAGGGGGGCCG
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                                                                                                                                                    cancer-associated DNA
                                                                                                                               cancer;
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gene; ds.
                                                                                                                                                                                                                          DNA; 1140
                                                                                                                               tumour
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                                                                                                                               tissue;
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                                                                                                                               human;
                                                                                                                               mammal;
                                                                                                                             cytostatic;
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13-OCT-2000; 2000US-0687576

12-OCT-2001; 2001WO-US32045

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08-DEC-2000; 2000US-0733742.
24-JAN-2001; 2001US-263957P.
16-MAR-2001; 2001US-276791P.
16-MAR-2001; 2001US-276888P.
06-MAR-2001; 2001US-281922P.
24-APR-2001; 2001US-281922P.
24-APR-2001; 2001US-288589P.
859 CATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGGCCCCTGCACCCTCCAGCT
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                                                           AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT
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01-MAR-1999; 01-MAR-2000;

99US-0122458

2000WO-US05226

TM,

Holtzman

DA,

Sharp JD,

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MILLENNIUM PHARM INC

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"TANGO 261"

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                                                                                                                                                                          Homo
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Best Loc
Matches
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266 and 267 useful as modulating agents of cellular processes,
for treating cancer -
TGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCAT
                                                                                                                                             CGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCA
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                                                                                       GCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAG
                                                                                                                         CGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCA
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Pred. No. 2.8e-120;
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                                                                                                   WPI; 200
P-PSDB; ;
                                                                                                                                                                                                                                                                                                                                                                                               cellular proliferation; cellular differentiation; cellular adhesion; yon Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disoase; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; brain herniation; carebral toxoplasmosis; parkinson's disease; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease;
                                                 262, 266
e.g. for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA clone encoding a human TANGO
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                          Disclosure;
                                                                           Novel human
                                                                                                                                                                                             01-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      multiple
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                                                                                                                                                                  (MILL-) MILLENNIUM PHARM
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DB; AAB18462.
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                                                                                                                                           TM,
                                               man and murine secreted and 267 useful as modul treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                      sclerosis; hydrocephalus; encephalitis; hepatic disorder;
                          Page -; 175pp; English
                                                                                                                                          Holtzman
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                                                                                                                                                                                             99US-0122458
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 6..764
                                                                                                                                                                                                                                                                                              /*tag= a
/product= "TANGO 261"
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                                                                                                                                           Fraser
                                                              ins designated TANGO agents of cellular p
                                                              0 216, 261,
processes,
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AAA75163-65 encode human TANGO 261 proteins. The

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                                                                            CAGCGCCACGTGCTACGGCAGCGGCGGGCGCATGGAGGGCCGCCGCCGCCCACCTACAGCGA 1113
                                                                                                                                                TGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCAT 1053
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Similarity 99.5%;
04; Conservative
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AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow. block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; brain herniation; latrogenic disease; hydrocephalus; brain herniation; latrogenic disease; latrogenic disease; latrogenic disease; latrogenic disease; parkinson's disease; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease;
                                                                                                                                                                                                                      Novel human and murine secreted proteins designated TANGO 216, 262, 266 and 267 useful as modulating agents of cellular procese.g. for treating cancer -
                                                                                                                                                                                                                                                                                           P-PSDB;
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note: the present sequence does not appear in the specification; it was
                                      1234
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Pred. No. 2.8e-120;
0; Mismatches 4;
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11-DEC-1998;
09-FEB-1999;
16-MAR-1999;
              Human neuron-associated proteins (NEUAP) can be used for for treating or preventing a disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, pick's disease, Huntington's disease, dementia and parkinson's disease. NEUAPs are also useful for treating other demyelinating diseases, bacterial and viral meningitis, prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebral palsy; muscular dystrophy; central nervous system; CNS; peripheral nervous system; PNS; myopathy; schizophrenia; actinic keratosis; arteriosclerosis; atherosclerosis; brisitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD; myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer; autoimmune disease; inflammation; acquired immunodeficiency syndrome; AIDS; Addison's disease; adult respiratory distress syndrome; AIDS; ankylosing spondylitis; amyloidosis; anaemia; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                              New human neuron-associated proteins and polynucleotides encoding the useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders
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Azimzai
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99US-0124687.
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CC palsy, neuroskeletal disorders, autonomic nervous system disorders, CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and cother neuromuscular disorders, peripheral nervous system disorders, CC other neuromuscular disorders, peripheral nervous system disorders, CC disorders including mood, anxiety and schizophrenic disorders, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, CC atherosclerosis, burstitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, hepatitis, mixed connective CC haemoglobinuria, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an autoimmune/inflammatory CC disease, adult respiratory distress syndrome, (AIDS), Addison's complications of cancer, hemodialysis, and extracorporeal circulation, complications of cancer, hemodialysis, and extracorporeal circulation, confections, and trauma. This sequence was given the Incyte ID no.
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Matches
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                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ActivinyInhibin activity, chemotactic/chemokinetic activity, heemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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Wang
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  sequence data
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GTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGG

GTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGG

GAGTTTGTTCAGATCATCATCAT - CGTGGTGGTGATGATGGTGATGGTGGTGATCAC Query Match Best Local S Matches 785

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21-JAN-2000;
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitites such as: Immune system suppression, ActivinyInhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Wang
Zhao
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                          specification
                                      C.N.S disorders.
Note: The sequence data
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DB; AAM40498.
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2000US-0552317.
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                                                                                                                                        Mouse cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
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                                                                            Mus musculus
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                                                                                                                                                                                                                                AGGTGAAAAGGCAG
                                                                                                                                                                                         standard; cDNA;
                                            Location/Qualifiers
20..844
/*tag= a
                                                                                                                           MIVR-1; Mechanically Induced Vascular Receptor
                                     /*tag= a
/product= "MIVR-1"
                                                                                                                                                                                                                                                1321
                                                                                                                                                          entry)
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                                                                                                       arteriosclerosis;
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The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC cardiac cell anti-apoptotic activity and fragments of the provided CC (MM_004338 and AQ177461. Also included are expression vectors, host CC (MM_004338 and AQ177461. Also included are expression vectors, host CC (MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule CC (MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its CC (MIVR-1) and thereby identifying a modulator. The cardiac cell anti-capoptotic molecules and nucleic acids of the invention are useful for CC (MIVR-1) and monitoring progression of such diseases and treating, diagnosing and monitoring progression of such diseases and cells e.g. cardiac hypertrophy, myocardial infarction, CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC encodes mouse MIVR-1.
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(PFIZ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
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CACGAGATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTAC
                                                                                                                                                 CTGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACAGCCAGGCCAGGAGG
                                                                                                                                                                                                               --TGGAATGCCGGAGCCACAGGTCTATGCCCCGCCCTCGGCCCACTGACCGACTCGCCTGTG
                                                                                                              CCGCCCTTCGCCCAGCGGAGCGCTTCCACCGTTCCAGCCCACCTATCCGTACCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                      740;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   878 BP; 179 A; 305 C; 247 G; 147
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.5
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RESULT 11
ABR12143/c

ID ABR12143;

XX
AC ABR12143;

XX
DE Human MIVR-1 homolog
XX Human; ss; MIVR-1;
XW cytostatic; cardiant
XW cytostatic; cardian
XW w0200216416-A2.
XX Landschulz
XX Landschulz
XX Landschulz
XX WNOYL nucleic acid n
PT Receptor-1 polypepti
XX PT Receptor-1 polypepti
XX Disclosure; Page 101
XX The invention relate
CC Cardiac cell anti-a;
CC NM_004338 and AQ177.
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     The invention relates to an isolated nucleic acid molecule encoding Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences AI761441.1, AI594390, NM_004338 and AQ177461. Also included are expression vectors, host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arterioscl. heart failure; AI761441.1.
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                                                                                                                                                               nucleic acid molecule
                                                                                                                                                                                                                                                                     BRIGHAM & WOMENS HOSPITAL PFIZER INC.
                                                                                                                                                                                                                                  Landschulz
                                                                                                                                             polypeptide, useful
                                                                                                              Page 101;
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                                                                                                                                          ng Mechanically Induced Vascular treating cardiovascular diseases
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RESULT 12
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ID AAA75
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AC AAA75
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DT 15-JA
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DE CDNA
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KW TANGC
KW CC11u

AAA75152

standard;

cDNA; 1713

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cDNA encoding

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murine TANGO

261

polypeptide

entry)

TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO cellular proliferation; cellular differentiation; c

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                           AAGGCAG
                                                                                                                            TCCTCCTTCCAGCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGA-GGGGACCCGGCT
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                                                      ACAGAAAGGACACCCTCTCTAGGGTCCCCCAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAA 1314
                                                                                                             CCCCCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAA
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Pred. No. 7.
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The present sequence encodes a murine TANGO 261 polypeptide. The CC specification also describes TANGO 266, TANGO 262, and CC TANGO 267. The TANGO polypeptides can be used to modulate cellular CC cellular adhesion. The proteins can be used to treat any von Willebrand CC cellular adhesion. The proteins can be used to treat any von Willebrand CC cellular adhesion, and cell trafficking and/or migration, modulate CC disorders, such as cancer, modulate cell adhesion in proliferative and/or function of cells that appear in the poliferative and/or function of cells that appear in the bone marrow, and leukocytes, disorders, atelectasis, pulmonary congestion or oedema, emphysema, and chronic bronchitis, bronchial asthma and bronchiectasis, intestinal CC disorders, spleen associated diseases, modulate renal disorders, treat calls and to treat bone and/or function of bone and cartilage calls and to treat bone and/or cartilage associated diseases or ovaries, cerebral oedema, bacterial and viral meningitis, Alzheimer's company and encephalus, brain herniations, introgenic considerase, inflammations, bacterial and viral meningitis, Alzheimer's considerers, hydrocephalus and encephalitis, and treat hepatic disorders, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                       Query Match
Best Local :
655 GAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGG
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes. e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; attelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC.
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                                                                                           GCTGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACAGCCAGGCCAGGAG
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573; Conserv
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                                                                                                                                                                                                                                                                                                            506 A; 438 C; 400 G; 369 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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Pred. No. 1.9e
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                                                                                                           TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disose; atelectasis; pulmonary congestion; cedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; anultiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                 Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                       ACAGAAAGGTCACCCCCTCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                              ACAGAAAGGACACCCTCTCTAGG 1277
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                                                                                                                                                                                                                                                         encoding a murine TANGO 261 polypeptide
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                                                           2..655
                                                                   Location/Qualifiers
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C and hematopoletic associated diseases and disorders, atelectasis,
C pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
CC asthma and bronchiectasis, intestinal disorders, spleen associated
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC as ischamic heart disease, modulate the proliferation, differentiation,
CC cartilage associated diseases or disorder. They may also be used to
CC treat disorders associated with the ovaries, and cerebral oedema,
CC hydrocephalus, brain herniations, latrogenic disease, ocrebral
CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
CC hydrocephalus and encephalitis, and treat hepatic disorders.
CC contest the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel
262,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA75166-68 encode murine TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1713 BP;
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                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                               178
                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ovel human and murine secreted 62, 266 and 267 useful as modul.g. for treating cancer -
                                                                                                                                                                                                                                                             61
                                                         GCACGAGATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTA
                                                                                                                                                                                                                                                                         GAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGG
               CCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGA
                                                                                                                          GCCCCCTTCATCCAGCGG-----AGCCGATTCCAACCCACCTACCCCTACCTGCA
                                                                                                                                                                                                                             GAGAGACGATGGACTGTCCTCGGACGGATGCCTCTGGCCCTCAGAGAGTACGGTGTCAGG
CCAGGGCCCTGCACCCTCCAGCTACGGGACCCTGAGCAACAGCTGGAGCTGAACCGGGA
                                                                                                                                                          GCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCA
                                                                                                                                                                                                                                                                                                                                                                                         572;
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page -; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holtzman
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83.7%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 464.6;
Pred. No. 3.4e
0; Mismatches
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                        Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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Disclosure;

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                    GTCCTCCTTCCAGCACCAGCAGAGCAGAGCAGTGGGCCCCTCCTTGCTGGAGGGGACCCGGCT
CTCCTCCTTCCAGCAGCAAAGTAACGGGCCATCCTCCCTGCTAGAGGGGACCCGGCT
                                                                                 CGGTGGGCGCATGGAGGGCCCCCCCCACCTACAGCGAGGTCATTGGCCACTACCCTGG
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                                                                                                                                                                                    GCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAG 1074
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83.7%; Pred. No. 3.4
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CC AAA75166-68 encode murine TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate CC cellular differentiation and/or modulate cellular adhesion. The CC disorder, regulate extracellular matrix structuring, cellular adhesion, CC modulate cell trafficking and/or migration, modulate cellular interactions, CC modulate the proliferation, differentiation and/or function of cells can be extracellular matrix structuring, cellular adhesion, CC modulate the proliferation, differentiation, and/or function of cells can appear in the bone marrow, and leukocytes, treat bone marrow, blood complimonary congestion or oedema, emphysema, chronic bronchitis, bronchial compliments of the condulate canal disorders, treat bone mascociated diseases, modulate renal disorders, spleen associated compliments of the condulate canal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation,
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Best Local Simi
Matches 572;
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                                                                                                                                     CCACCACACACACACGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGAGAAGAAA 1254
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Similarity 83.7%;
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Copyright (c) 1993 - 2003 Compuc
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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ω	Sequence 3, Appli	11	Sequence 1, Appli	Sequence 3, Appli	Sequence 7, Appli	Patent No. 5352575	Sequence 10, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl	Sequence 16, Appl	Sequence 3, Appli	Sequence 16, Appl

ALIGNMENTS

Sequence 7, Application US/09091952A Patent No. 6458532 GENERAL INFORMATION: TELEX: <Unknown> INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor COMPUTER READABLE FORM: MEDIUM TYPE: Diskette APPLICANT: Detera-Wadleigh, S Gershon, Elliot S. NUMBER OF SEQUENCES: 197 COUNTRY: USA ZIP: 94111-3834 CITY: San Francisco STATE: CA . COMPUTER: IBM Compatible TELEFAX: (415) 576-0300 Esterling, Lisa E. OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness LENGTH: 921 base pairs Sanders, Alan R. Berrettini, Wade Yoshikawa, Takeo Goldin, Lynn R. Badner, Judith A. Gershon, Wade H Sevilla 015280-297100US

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US-09-091-952A-6
; Sequence 6, Application
; Patent No. 6458532
; GENERAL INFORMATION:
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                 TITLE
                                                                                                               APPLICANT: Detera-Wadleigh, S
Gershon, Elliot S.
                                                                                                                                                                                                                                                          TOPOLOGY:
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LOCATION: 1...921
OTHER INFORMATION:
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Sanders, Alan R.
Esterling, Lisa E.
Enterling, Lisa E.
INVENTION: Chromosomal Markers and
Tests for Manic-Depressi
                                                    Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
                                                                                                Badner, Judith A.
                                                                                                            Gershon,
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US97/19381 FILING DATE: 28-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ fo CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE TADDRESSE: Townsend and Townsend and Crew LL:
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC
                                                                                                                                                  ATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCC 625
                                                                                                                                                                                        CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCATCGTCGTGGTGGTC 340
                                                            TTCATCAGCCGGCACAGCCAGGGGGGGGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGC 685
                                       TTCATCAACCGCCCGAACCAGAGCCGGAGGCCGGGAGGACGGGCTGCCGCAGGAAGGGTGC
                                                                                                                                                                                                                                                                  482;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 5595...5685 OTHER INFORMATION: amp
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 452...505 OTHER INFORMATION: alte
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LOCATION: 116...1036
OTHER INFORMATION: Clone
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OTHER INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, Timothy L. REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/029,278 FILING DATE: 28-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/091,952A FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                  Conservative
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73.1%;
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                                                                                                                                                                                                                                                              Score 352.2; DB 4;
Pred. No. 7.2e-58;
0; Mismatches 168;
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US-09-091-952A-8
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                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.

CURRENT APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-199
CLASSIFICATION CUMBER: US/09/091,952A
FILING DATE: 19-Apr-199
CLASSIFICATION WINDER: US 60/029,278
APPLICATION NUMBER: US 60/029,278
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: SGITTANTON:
NUMBER: SGITTANTON:
NUMBER: METERS PCT/US97/19381
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ADDRESSEE: Townsend and
STREET: Two Embarcadero
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Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
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                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarca
CITY: San Francisco
             NAME: Smith, Timothy L. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                              STATE: CA
REFERENCE/DOCKET NUMBER: 015280-297100US
                                                                                                                                                                                                                                                                                                                                                                                                            OF SEQUENCES:
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                                                                                                                                                                                                                                                                                               94111-3834
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Yoshikawa, Takeo
Yoshikawa, Alan R.
Sanders, Alan R.
Esterling, Lisa E.
Esterling: Chromosomal Markers and
Tests for Manic-Depressi
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                 , 367
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Best Local
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INFORMATION FOR SEQ ID NO: 8:
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OTHER INFORMATION: Cl
spliced coding region
SEQUENCE DESCRIPTION: SEQ
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CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCATCGTCGTGGTGGTC
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                                                                                                             CCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACATC 985
                                                                                                                                                                                                         CTGTCAGACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC
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                                              ACTCGGGCATCAGTGCAAGCACCTGCAGCAGTAACGGGAGGATGGAGGGGCCACCCCCC
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                                                                      CTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCTGCACCCTGCAGCTCCGGGAC
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                                                                                                                                                                                                                                                                                                                                                        CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC
                                                                                             LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..
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TELEFAX: (415) 576-0300
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Pred. No. 3e-45;
0; Mismatches 143;
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RESULT 4
US-08-08-04-227C-7/c
; Sequence 7, Application
; Patent No. 5876991
; GENERAL INFORMATION:

US/08804227C

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Best Local Similarity
Matches 234; Conserv
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                                                                                                                                                                                                            19499 CTCGGGTGCGGAACGTCCCGGGAGCCGCGGCGAGCGTCCGGCGGGGGGCGTCGGGGGC 19440
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APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
APPLICANT: Sutton, Kimberly L.
APPLICANT: POLYKETIDE SYNTHASE GENES
                               19319 GGCCGCGCGCGCAGGTCGAGCCGCACGGGCAGGGCCGGGCTCGGGCCCGGGT-CAGCG
                                                                                                                                                   19439
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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CITY: INDIANAPOLIS
245 CCCCGCGCGCCCCCGGGAACTTGGCGGCGACCCGAGCCCGGGCGAGCCGGGGGCGCGCCTCC 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                          GCAGCGCGCCCCCCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCACTGCCGACGC
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                                                                                         GCGGGCGTCCGCCGGTACGCCGGCCAGGTCACGCAGGACCTCCGGGAGAGCGGTGGCACC 19320
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LILLY CORPORATE CENTER
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IBM Compatible
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14046..20036
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31329..36071
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Pred. No. 0.00018;
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JS-08-804-198-1
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                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                       FEATURE:
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CITY: INDIANAPOLIS
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            NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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LILLY CORPORATE CENTER
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             36155..41830
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31329..36071
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14046..20036
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US-08-690-473-1/c
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Patent No. 587692
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Best Local Similarity 49.2
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Leopardi, Rosario
APPLICANT: ROIZMAN, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
                                           APPLICATION UMBER: US/08/690
EILING DATE: 26-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
             TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                     ARCD: 239
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Pred. No. 0.00018;
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; TYPE: DNA; ORGANISM: HERPES US-09-259-821A-1
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-690-473-1
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                                                                                                                                                                                                              Sequence 1, Application US/09259821A
Patent No. 6210926
GENERAL INFORMATION:
APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERRES SIMPLEX VIRUS ICP4
FILE REFERENCE: ARCD:317
 Best Local Similarity Matches 239; Conserv
                             Query Match
                                                                                                                 SEQ ID NO 1
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                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/259,821A CURRENT FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: 08/690,473 PRIOR FILING DATE: 1996-07-26
                                                                                                                             NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn V
                                                                                                   LENGTH: 4257
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48.8%;
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Score 67.6; DB 4;
Pred. No. 0.00016;
0; Mismatches 249;
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Pred. No. 0.00016;
0; Mismatches 249
  249;
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RESULT 8
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Patent No. 6218103
                  TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                     NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: AR.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
ADDITION MINISTED: INC/NS/AA 66
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APPLICANT: Roizman, Bernard
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                  APPLICATION NUMBER: US/08/843,659
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
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         LENGTH:
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RESULT 9
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                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOTOGPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
EILING DATE: 02-JUNE-1995
CLASSIFICATION: 435
                                                                                                                      COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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Best Local Similarity
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz 6 No. 5821339ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                   APPLICANT: Yeh, Lily
TITLE OF INVENTION: Composition
TITLE OF INVENTION: Infections
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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TOPOLOGY: lin
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Pred. No. 0.00016;
0; Mismatches 249
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CLASSIFICATION:

05-MAY-1993

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GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                          Sequence 16, Application US/09128155
Patent No. 6117654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36.317
REFERENCE/DOCKET NUMBER: DFCI-0029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
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MOLECULE TYPE:
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TYPE: nucleic acid
STRANDEDNESS: double
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les 239; Conserv
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                                                                                                                                                                                                                                                                                   GGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAG
                                                                                                                                                                                                                                                                                                                                             GCCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGCC 457
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                                                                                        SOFTWARE: PatentIn SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                            APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
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CURRENT FILLING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILLING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILLING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                              APPLICANT:
                                                    LENGTH: 44
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21828 GGGGGTGCAGTGGGGTTGGGTGGGGTGGGTNNNACNNNNNCNCCCCCCCCC 21887
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LOCATION: (1)...(152331)
OTHER INFORMATION: n = A
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TYPE: DNA
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OTHER INFORMATION: CDC 1551
                   FEATURE:
                                   ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                            WHITE, Owen R.
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                                                                                                           Ver. 2.1
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Pred. No. 0.00051;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-845-998-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 3936851 CGGTGATATTGCCGCCGTTGCCGCCGGCTCCCGGCCGCCGCCGGCACCACCTTGACCAC 3936792
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08845998 Patent No. 5879892 GENERAL INFORMATION:
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US-09-103-840A-2
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Best Local Similarity 46.1%;
Matches 219; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van Baren, Nicola
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
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                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks,
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Boon, Thierry
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                                                                                                                                                                                          Floppy disk
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                    L0461/7008
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                                                                                                                                      Sequence 7, Application US/09206537
Patent No. 6130052
GENERAL IMPORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
                                                                                                                                                                                                                                                                     US-09-206-537-7/c
                                                                                                                                                                                                                                                                                          RESULT 13
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Best Local Similarity 49.5%;
Matches 218; Conservative
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TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
                                                                         NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
                         STREET: 600 A
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                      AGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGA
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                                                         600 Atlantic Avenue
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                                                                                                                   LEUKEMIA ASSOCIATED GENES
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Pred. No. 0.00074;
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COMPUTER READABLE FORM:

TYPE:

OPERATING SYSTEM: COMPUTER:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS Floppy disk

PatentIn Release #1.0, Version

#1.

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RESULT 14
US-09-430-854-7/c
; Sequence 7, Application US/09430854
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US-09-206-537-7
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
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mes 218; Conserv
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                                                                                                                                                                                 :: (617)720-3500
(617)720-2441
OR SEQ ID NO: 7:
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Pred. No. 0.00074;
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Matches 218
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INFORMATION FOR SEQ ID NO: 7:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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ADDRESSEE: Wolf, Greenfield
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ZIP: 02210
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                                                                                      TGCGACAGGTGGCCCAGGCTGTGCATATGCGGGTGAGGGTGCGCGGAGCCGCCCAGGAGC
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Lucas, Sophie
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; Pred. No. 0.00;
0; Mismatches
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                                                                                                                                                                                                                                                                                                        . 0.00074;
ches 220;
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US-08-795-430-48
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US-08-795-430-48/c
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
OA/ERE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/08795430 Patent No. 6130071
                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                               NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2896
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-0448
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               MOLECULE TYPE:
                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14 NOV-1994
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor
TITLE OF INVENTION: Protein and Gene, Mutants Thereof,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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CITY: Chicago
STATE: Illinoi
COUNTRY: Unite
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                                     TOPOLOGY:
                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                   Query Match 4.8%;
Best Local Similarity 49.4%;
Matches 164; Conservative
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                                                CCCTCCCCTCTCACTCTCCCTCGGAAGCCGTCTCCCCTGGAGCTCCCCGGTTTCCCTCGCCT 2238
                                                                                                  CCTCCCGGGGGGCCCACCTCCCCCAGCCCCC 2206
                         CCCCCGGCCGCGCCCGAGCCCCCGCGCGCCCC 390
                                                                           GCCTCCCCGGCGGGGCCTCCTGCATGCGGGGCCCCAGCTCCGGGCGGCCGGGCCGAGCC 358
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Pred. No. 0.001;
0; Mismatches 168;
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Search completed: March 17, 2003, 14:12:34 Job time: 1067.57 secs

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Result
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Maximum DB seq
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US00_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

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US-10-000-256A-32
US-09-934-249-16
US-09-934-249-18
US-09-976-740-48
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Sequence 1, Appli
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Sequence 55, Appl
Sequence 71, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 57, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 48, Appl
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NGAGGCTCAGCCCC 120	Indels 0; Gaps 0; AGGAGGAGGAGGCGG 60 	Length 1321;		sequence 15, Appl Sequence 17, Appl Sequence 17, Appl Sequence 47, Appl Sequence 45, Appl Sequence 45, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl	Sequence 45, Appl Sequence 45, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl	Sequence 1351, Ap Sequence 1, Appli Sequence 292, App Sequence 529, App Sequence 3950, Ap Sequence 47, Appli Sequence 8, Appli

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Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Lee, Richard T.
APPLICANT: Turi, Thomas G.
APPLICANT: Trui, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 3
ILENGTH: 861
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(861)
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FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT APPLICATION NUMBER: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PRICICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/474,073
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
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PRIOR APPLICATION NUMBER: 09/474,072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND
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US-09-796-753-55
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LENGTH: 969
TYPE: DNA
ORGANISM: Homo:
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Best Local Similarity
Matches 805; Conserv
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
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OR APPLICATION NUMBER: 09/606,565

OR FILING DATE: 2000-06-29

OR APPLICATION NUMBER: 09/606,317

OR FILING DATE: 2000-06-29

OR APPLICATION NUMBER: 09/665,666

OR APPLICATION NUMBER: 09/665,666

OR FILING DATE: 2000-09-20
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R APPLICATION NUMBER:
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FILING DATE: 2000-07-31
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FILING DATE: 2000-06-22
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                                                               TGACCTGATGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCAT
                                                                                                                   GCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAG
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CAGCGCCACGTGCTACGGCAGCGGCGGCGCCATGGAGGGGCCGCCGCCCACCTACAGCGA
                                                                                                      GCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAG
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Pred. No. 4.5e-144;
0; Mismatches 3;
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US-10-098-841-71
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CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-21
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                                                                                                                                                                                                                                                                                                                    SOFTWARE: pt_F
SEQ ID NO 71
LENGTH: 1066
                                                                                                                                                          Query Match 59.8%;
Best Local Similarity 99.2%;
Matches 794; Conservative
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NO. US20020197679Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
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APPLICANT:
APPLICANT:
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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 642 GCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                               582
                                                                                               113
                             TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA 641
                                                                                                            CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGATGATGGTGATGGTGGTGGTGG 581
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Qian, Xiaohong
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Wehrman, Tom
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Chen, Rui-hong
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Wang, Jian-Rui
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                                                                                                                                                           Mismatches
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APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
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US-09-934-249-12
                                                                                                                                                                                                                              APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Kat
APPLICANT: Tuni, Thomas G.
APPLICANT: Thompson, John
APPLICANT: Kennedy, Scott
                                                                                                                                                                                                                                                                                                         Sequence 12, Application UPatent No. US20020115081A1 GENERAL INFORMATION:
                                         LENGTH: 87
              ORGANISM: Mus
FEATURE:
NAME/KEY: CDS
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RESULT 6
US-10-000-256A-32
; Sequence 32, Application US/10000256A
; Publication No. US20030039983A1
; GENERAL INFORMATION:
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US-09-934-249-12
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Best Local Similarity
Matches 740; Conserv
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                                                                                                                                         TCCTCCTTCCAGCAGCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTC
                                                                                                                                                                                                                            CTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGC
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                                                                            CAGAAAGGACACCCTCTCTAGGGTCCCCCAGGGGGGGCCG
                                                                                                                CACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAA
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                                                                  CAGAAAGGTCACCCCCTCTAGGAGTGGGGGCCGGGGCG
                                                                                                      CATCACTCGCACATTGCCCCACTGGA---
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84.3%;
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Pred. No. 1.2e-108;
0; Mismatches 111;
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                                                                                                     -GAACAAGGAGAAGGAGAAA
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; LENGTH: 1583
; TYPE: DNA
; ORGANISM: HOMO s
US-10-000-256A-32
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Seiru
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Re
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
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SOFTWARE: Patent
SEQ ID NO 32
FENGTH: 1583
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Best L
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Local Similarity
hes 591; Conserv
                                             CCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGCGGTAGGTGAAAAGGCAG
                                                                                                                                         TGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGGCGCATG
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                                                                                                                                                                                                      GAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTAG
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                                                                                              ATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACAC
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Pred. No. 1.9e-103;
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; Sequence 14, Application US,
patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Kat
APPLICANT: Turi, Thomas G,
APPLICANT: Thompson, John
APPLICANT: Kennedy, Scott

Н

US/09934249

Turi, Thomas G. Thompson, John I Kennedy, Scott I Landschulz, Katherine

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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS FILE REFERENCE: P0738/7001/ERP/KA CONDITIONS FILE COURTENT APPLICATION NUMBER: U5/09/934,249 CURRENT FILING DATE: 2001-08-21 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: US 60/227,159 PRIOR FILING DATE: 2000-08-22 NUMBER OF SEQ ID NOS: 17 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 14 LENGTH: 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: unsure
; LOCATION: (639)...(639)
; OTHER INFORMATION: a, c,
US-09-934-249-14
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US-09-766-753-57
Sequence 57, Application US/09796753
; Publication No. US20030027998A1
; Publication No. US20030027998A1
; GENERAL INFORMATION:
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             APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
                                                                                                                                                                                                                                                                                                                                                                                                                   1016
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PRIOR FILLING DATE: 199-224
PRIOR APPLICATION NUMBER: 09/224
PRIOR APPLICATION NUMBER: 09/256
PRIOR FILLING DATE: 1999-02-26
PRIOR FILLING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/31
PRIOR APPLICATION NUMBER: 09/31
PRIOR APPLICATION NUMBER: 09/31
PRIOR FILLING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/33
PRIOR APPLICATION NUMBER: 09/34
PRIOR FILLING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR ETLING DATE: 1999-09-30
PRIOR PRICING DATE: 1999-09-30
PRIOR PRICING DATE: 1999-12-23
PRIOR PRICING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR APPLICATION NUMBER: 09/474,072
                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (2)...(652)
US-09-796-753-57
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PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/2
PRIOR APPLICATION NUMBER: 09/2
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PRIOR TILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/V
PRIOR EILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/1
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                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                              FEATURE:
                                              655 GAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGG
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FILING DATE: 2000-03-01
APPLICATION NUMBER: 09/
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APPLICATION NUMBER:
FILING DATE: 2000-0
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83.9%;
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                                                                                                                    Score 466.2; | Pred. No. 4.1e
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                                                                                                                         DB 9;
. 4.1e-80;
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                                                                                                                                                      Length 1713;
                                                                                                                              Gaps
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GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott F.
APPLICANT: Kennedy, Scott F.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
DBIOD ADDITOTION NUMBER: US/09/934,249
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                                                                                                                                                        SEQ ID NO 16
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DAYE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3
                                        NAME/KEY: unsure LOCATION: (6477)...(6477) OTHER INFORMATION: c or t
NAME/KEY: unsure
LOCATION: (6837)...(6837)
OTHER INFORMATION: a or c
                                                                                         TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                     LENGTH: 8093
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                                                                                                                                                                     Version 3.0
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APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Turi, Thomas G.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                           NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows
SEQ ID NO 15
                                                                                                                                                                                                                                                                            Sequence 15, Application U Patent No. US20020115081A1
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Best Local Similarity
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LENGTH: 475
TYPE: DNA
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                                               Version
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Pred. No. 8.2e-58;
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; PRIOR APPLICATION NUMBER: 08/420,856; PRIOR FILING DATE: 1995-04-12; PRIOR APPLICATION NUMBER: 08/346,731; PRIOR FILING DATE: 1994-11-21; NUMBER OF SEQ ID NOS: 12485; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 3464; LENGTH: 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3464, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.9%;
Best Local Similarity 85.5%;
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William
NAME/KEY: misc feature
LOCATION: (225)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (279)
                                                                                  NAME/KEY: misc feature
LOCATION: (103)
OTHER INFORMATION: n equals
                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA
                                                                                                                                          FEATURE:
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Pred. No. 1.4e-56;
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; LENGTH: 4020
TYPE: DNA
; ORGANISM: Orf virus strain NZ-2
US-09-796-679-5
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                                                                                                                                           SOFTWARE: PatentIn
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09796679 Publication No. US20030013076A1
     Matches
                  Query Match
Best Local Similarity
                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/NZ97/00040
PRIOR ETLING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: NZ 286284
PRIOR EILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                    APPLICANT: University of Otago
TITLE OF INVENTION: Parapoxvirus vectors
FILE REFERENCE: 23607 MRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/796,679
CURRENT FILLING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/155,421
PRIOR FILING DATE: 1998-09-29
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Robinson, Anthony J APPLICANT: Lyttle, David J
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LOCATION: (368)
COTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (349)
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   220;
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   0;
Score 78; DB 9; Le
Pred. No. 2e-06;
0; Mismatches 215;
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Pred. No. 2.9e-26;
0; Mismatches 1
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                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-09-976-740-48
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
                                                                Query Match 5.7%;
Best Local Similarity 53.0%;
Matches 206; Conservative
                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: AIJONA, ANIBAL A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/976,740 CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                           ORGANISM: Oryctolagus FEATURE:
                                                                                                                                                                                                                            LENGTH: 2561
TYPE: DNA
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574 GCGGCGAGGGGTGCATGCTTGTTGGCTGCCGGTGTTGGCCGTCTGGCGGGTGGAAGGCGGGT
                  56 GGCGGCGGCGGCGGCGGGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCA 115
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                                                                   0;
                                                                  Score 75.4; DB 9;
Pred. No. 6e-06;
0; Mismatches 181;
                                                                                                   Length 2561;
                                                                   Indels
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116 GCCCCGGCGCGCGCGCCCCCCCCCCCCCCCCCCCGGACGCCCACCCGGGCAC

816

CGGGGGAGCGGCGCGCGGCGGCGCGCCAGGGGCCGCGCCCGCTGCGCGCGGGG

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RESULT 14
US-10-023-529-48/c
US-10-023-529-48/c
; Sequence 48, Application US/10023529
; Patent No. US2002012938BA1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Ann M.

APPLICANT: Law, Simon M.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: APHEROSCILEROSIS

FILE REFERENCE: 10797-004001

CURRENT FELLING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                            Query Match 5.7%;
Best Local Similarity 53.0%;
Matches 206; Conservative
                                                                                                                                                                                                                                                                            SEQ ID NO 48
LENGTH: 2561
                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (246)...(1895)
                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Oryctolagus cuniculus
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                                                                                              Score 75.4; DB 12; Pred. No. 6e-06;
                                                                              Mismatches 181;
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GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: ALJONA, ANIBALA.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATTEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,523

CURRENT APPLICATION NUMBER: US/09/616,289

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR APPLICATION NUMBER: US/09/517,849

PRIOR APPLICATION NUMBER: US/09/517
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US-10-023-523-48/c
Sequence 48, Application US/10023523; Patent No. US20020152485A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-10-023-523-48
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Best Local Similarity 53.0%;
Matches 206; Conservative
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SOFTWARE: FRASTSEQ for Windows Version 4.

SEQ ID NO 48

LENGTH: 2561

TYPE: DNA

ORGANISM: Oryctolagus cuniculus
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116 GCCCCGGCGCCAGCCCCGCCGCCCAGCCCATTTTCCGGACGCCACCCGCGGGCAC 175
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Pred. No. 6e-06;
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Search completed: March 17, 2003, 18:33:21 Job time: 126.606 secs

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Result
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION FEATURES COMMENT RESULT 1 AL578575/c source M Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebr
Mammalia; Eutheria; Primates; Catarrhini; Homin
1 (bases 1 to 1007)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cunA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genos EST prime, mRNA sequence. AL578575 AL578575 AL578575 LTI_NFL006_PL2 human /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDDK001YC24"
/clone_lib="LTI_NFL006_PL2"
/closue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand was primed with a NotI-oligo(dT) primer. Five prime Location/Qualifiers 1. .1007 GI:12942781 Homo ďď bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CSODKOO1YC24 3 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Web : www.genoscope.cns.fr. cDNA end

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9; Mismatches 10;
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Email:
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Mammalia; Eutheria;
1 (bases 1 to 967)
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National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                    found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.
                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                   GGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAA 1243
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/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH1DB (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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D; Mismatches 7;
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                                                  GGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACA 706
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1046)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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5', mRNA sequence.
BM922276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/note="organ: pooled brain, lung, testis; Vector:
/note="organ: pooled brain, site_2: EccRV (destroyed); RNA
pcMV-SpORT6; Site_1: NotI; Site_2: EccRV (destroyed); RNA
source anonymous pool of 6 male brains, age for ange 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

a 391 c 298 g 150 t 2 others
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/clone="IMAGE:5754437"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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95.8%;
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Pred. No. 2.1e-127;
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C_115 Homo sapiens cDNA cLone IMAGE:5754437
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AGENCOURT_8825282 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204609 5', mRNA sequence.
                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13626 row: c column: 10
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 916)
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EST.
                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                quality sequence stop:
                          /clone_lib="Lupski_sciatic_nerve"
                                          /db_xref="taxon:9606"
/clone="IMAGE:6204609"
/tissue_type="sciatic nerve"
            /sex="male"
                                                                       /organism="Homo sapiens"
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              GGCCA--CTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAGTGGGCCGCCCTCC
                                                       CGTGCTACGGCAGCGGCGGC-GCATGGAGGGGCCGCCCCCCCCACAGAGCGAGGTCATC 1120
                                                                                                GATAGTGCCAAGGCTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technologies.
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/lab_host="DH10B"
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Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
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AL558881 LTI_NFL008_TC2
prime, mRNA sequence.
AL558881
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="T cells from T cell leukemia"
/note="Vector: pcwVSPORT 6; Site_1: NotI; Ist strand cDNA
/note="Vector: pcwVSPORT 6; Site_1: NotI; Ist strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcwVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA rax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://fulllength.invitrogen.com"
248 c 289 g 161 t
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/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LTI_NFL008_TC2"
/sex="male"
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Eutheria;
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/tissue_type="placenta"
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REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS COMMENT SOURCE ORGANISM EST Homo sapiens

ACCESSION DEFINITION Eukaryota; Metazoa; Chordata; Ci Mammalia; Eutheria; Primates; Ca 1 (bases 1 to 898) Li,W.B., Gruber,C., Jessee,J. ar Full-length CDNA libraries and n Unpublished (2001) AL558882 LTI_NFL008_TC2 prime, mRNA sequence. AL558882 AL558882.1 GI:12903838 Jessee,J. and Polayes,D. braries and normalization Homo 898 sapiens Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA linear EST 16-FEB-2001 ns cDNA clone CS0DJ015YF12 5

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/sex="male" /---
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/note="Tells from T cells from T five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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   Nature 409
21085660
                                                                 Functional
                                                                                               and Hayashizaki, Y.
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                                                             annotation of a full-length mouse cDNA collection
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Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for firsthor Jatasia.
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                                                                                                                                   Similarity
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/db_xref="MGD:MGI:1929600"
/db_xref="MGD:MGI:1929600"
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VRAPPNRTIFDSDLISTMLGGPCPPSSNSGISATCYSSGGRMEGPPPTYSEVIGHYP
GSSFQHQQSNGPSSLLEGTRLHHSHIAPLENKEKEKQKCHPL"
a 459 c 374 g 173 t 1 others
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/clone_lib="RIKEN full-length enriched mouse
/dev_stage="adult"
391. 1173
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/strain="C57BL/6J"
/db_xref="FANTON_DB:2210418102"
/db_xref="MGD:MGJ:1907457"
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VERSION KEYWORDS

BC023092
Mus musculus,
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ACCESSION

SOURCE

LOCUS DEFINITION

Nedd4 WW

1079 bp binding p

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IMAGE: 3989996

HTC 07-AUG-2002

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AGAAGGAGAAACAGAAAGGTCACCCCCTCTAGGAGTGGGGGGCCGGGGCG
                                                           GGACCCGGCTCCATCACTCGCACATTGCCCCACTGGA--
                                                                                        GCTACGGCAGCGGCGCGCATGGAGGGGCCGCCCCACCTACAGCGAGGTCATCGGCC 1124
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                           AGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCG
                                                                                                                      ACTACCCTGGCTCCTTCCAGCACCAGCAAAGTAACGGGCCATCCTCCCTGCTAGAGG
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                                                                                              TGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACAGCCAGGCCAGGAGGA
                                                                                                              TTCAGATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGATCACGTGCCTGC
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                                          GAGACGATGGACTGTCCTCGGAAGGATGCCTCTGGCCCTCAGAGAGTACGGTGTCAGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 36 Row: h Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-FEB-2002) National Institutes of Health, | Gene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
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                                                                                                                                                                                                                                                                                                                                        Similarity
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor metastatized to lung arose spontaneously from a senescent normal mamm (clonal) outgrowth infected with the virus MMTV./clone_lib="NCI_GGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6"
341 c 289 g 178 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/map="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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84.5%;
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Pred. No. 4.6e-101;
D; Mismatches 109;
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                                                                                                                      CDNA Library preparation: Dr. M. Bento Soares, University of Iow CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                         Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 782)
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/organism="Homo sapiens"
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/clone="IMAGE:5834635" /clone_1ib="NCI_CGAP_ED1" /tissue_type="Chondrosarcoma"

/db_xref="taxon:9606"

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RESULT 12
BQ636742 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 CTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  782 GAGAGCACAGTGTCAGCAAACGGAATCCCAGAGCCGCAGGTNTACGCCCCGCCTCGCCCC 723
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                                                                            GGGGCTGCGTAGGTGAAAAGGCAG 1321
                                                          GGGGTTGCGTAGGTGAAAAGGCAG 159
                                                                                                                  AGCAAAGAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCT 183
                                                                                                                                 AGCAAAGAGAAGAGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCT 1297
                                                                                                                                                                                  CTGGAGGGGACCCGGCTCCACCACACACACACCCCCTAGAGAGCGCAGCCATCTGG
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                                                                                                                                                                                                                                                  ATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTAGTGGGCCGCCCCCTTG 1177
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617; Conserv
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/lab_host="DH10B (Life Technologies)"

/note="Organ: Left pubic Bone; Vector: pT7T3-Pac (Pharmacla) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EDI is a normalized cDNA library containing the following tissue(s): Chondrosarcoma cell line CS5. The library was constructed according to Bonaldo First strand cDNA synthesis was primed with an oligo-dr ligated to an EcoR I adaptor, digested with Not I, and cligated to an EcoR I adaptor, digested with Not I, and oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is sequence that for this library tag sequence that is
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223 c 271 g
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TAG_LIB=UI-H-ED1
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98.9%;
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Pred. No. 2.4
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nes 7;
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871 AGACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGA 930
                                                                                                source
                                 CCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCCACCATCTCGCTGTC
                                                  608;
                                                                                                                                                                                                                                                                                                                            Similarity
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Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts

Mol. Vis. 8 (4), (2002) In press
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hd13h06.yl Human Retina
"~~~ sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Section on Molecular Structure and Function National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BQ636742.1
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                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: Eye; Vector: pSPORT1, Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the psport vector (Life Technologies) was constructed at the protocols of the Superscript plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First primer adapter [5'-pGACTAGTTCTAGTTCTGATCGGCACGCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hd13h06"
/clone_lib="Human Retina cDNA (Un-normalized, unamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                          46.0%;
99.8%;
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Pred. No. 4.7e-99;
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DB 14;

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                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2368 row: h column: 14
High quality sequence stop: 627.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 890)
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                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                168
       /Clone_lib="NH_MCC_il0"
/Clone_lib="NH_MCC_il0"
/tissue_type="ductal carcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Site_2: ECORI; cDNA made by oligo-dT priming the following 5' adaptor: GGCACAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6209341"
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Primates;
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110 Homo sapiens
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93.5%;
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REFERENCE AUTHORS TITLE RESULT 14 BQ575741/c LOCUS VERSION KEYWORDS SOURCE ACCESSION DEFINITION ORGANISM JOURNAL Bukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 729) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov BQ575741 729 bp mRNA UI-H-EZ1-bbg-h-14-0-UI-S1 NCT_CGAP_Ch2 HC UI-H-EZ1-bbg-h-14-0-UI 3', mRNA sequence. BQ575741 GI:21479058 EST. Homo sapiens Gene Index Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Homo Anatomy linear sapiens EST 1 19-JUN-2002 clone

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Library

preparation: Arrayed by: 1

Dr. M. Bento Soares, University of Iowa Dr. M. Bento Soares, University of Iowa

Gitelis/ Rush Presbiterian, Dept. of

Tissue Procurement: Dr. Steven

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Seq primer: M13 FORWARD
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//ALD_host="Part Pelvis; Vector: pT7T3-Pac (Pharmacia)
//ALD_host="Part Pelvis; Vector: pt. Pac (Pharmacia)
//ALD_host="Part Pelvis; Vector: p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_TISSUE-grade-2-chondrosarcoma
TAG_SEQ-ATCTAATATG"
213 c 253 g 162 t
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/dev_stage="Adult"
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/clone_lib="NCI_CGAP_Ch2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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AUTHORS
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Tissue Procurement: Dr. Greeg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 730)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                                                                                               //ADL/host="Diffusion (Ilfe Technologies) (Tl phage resistant)"
//ADL/host="Torgan: eye; Vector: pTTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-E01 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
support of site. Double stranded cDNA was ligated to an EcoR I
into pTTT3-Pac vector. The oligonucleotide used to prime
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
Discovery in the Visual System, supported by National Eye
TAG. ITHR-TETS-TOT
                                                                                                                                                                                                                                  TAG_SEQ=CGCGTATACC*
210 c 251 g
                                                                                                                                                                                                                                                                                                    TAG_LIB-UI-E-EO1
TAG_TISSUE-human fetal eye
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/clone_lib="UI-E-E01"
/tissue_type="fetal eye"
/dev_stage="fetal"
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                                                   42.8%;
Score 564.8;
Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                             251 g
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CGGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
                                 CGGCCCACCGACCGCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTC
                     ATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCCAGGGGGGC 1291
                                                                                                                                        ATCTGGAGCAAAGAAGAATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGC
                 191
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